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1 ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCGGCTGCTGC 60  
-----+-----+-----+-----+-----+-----+  
TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAAGGGGTGGACGGGGCCGACGACG  
M W K W I L T H C A S A F P H L P G C C  
61 TGCTGCTGCTTTTTGTTGCTGTTCTTGGTGTCTTCCGTCCCTGTCACCTGCCAAGCCCTT 120  
-----+-----+-----+-----+-----+-----+  
ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA  
C C C F L L L F L V S S V P V T C Q A L  
121 GGTCAGGACATGGTGTCAACAGAGGCCACCAACTCTTCTCCTCCTCCTCCTCCTCCT 180  
-----+-----+-----+-----+-----+-----+  
CCAGTCCTGTACCACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGAGGA  
G Q D M V S P E A T N S S S S S F S S P  
181 TCCAGCGCGGGAAGGCATGTgCGGAGCTACAATCACCTTCAAGGAGATGTCCGCTGGAGA 240  
-----+-----+-----+-----+-----+-----+  
AGGTGCGCGCCCTTCCGTACAcGCCTCGATGTTAGTGGAAGTTCTCTACAGGCGACCTCT  
S S A G R H V R S Y N H L Q G D V R W R

MATCH WITH FIG. 1B

FIG.1A



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MATCH WITH FIG. 1A

241 AAGCTATTCTCTTTACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG 300  
-----+-----+-----+-----+-----+-----+  
TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCC  
K L F S F T K Y F L K I E K N G K V S G  
301 ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360  
-----+-----+-----+-----+-----+-----+  
TGGTTCTTCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA  
T K K E N C P Y S I L E I T S V E I G V  
361 GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACTC 420  
-----+-----+-----+-----+-----+-----+  
CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG  
V A V K A I N S N Y Y L A M N K K G K L  
421 TATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480  
-----+-----+-----+-----+-----+-----+  
ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT  
Y G S K E F N N D C K L K E R I E E N G

MATCH WITH FIG. 1C

FIG.1B



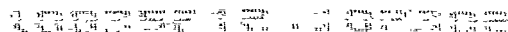
20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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MATCH WITH FIG. 1B

481 TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540  
-----+-----+-----+-----+-----+-----+  
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC  
  
Y N T Y A S F N W Q H N G R Q M Y V A L  
  
541 AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600  
-----+-----+-----+-----+-----+-----+  
TTACCTTTTCCTCGAGGTTCCCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGAGACGAGTG  
  
N G K G A P R R G Q K T R R K N T S A H  
  
601 TTTCTTCCAATGGTGGTACACTCATAG 627  
-----+-----+-----  
AAAGAAGGTTACCACCATGTGAGTATC  
  
F L P M V V H S \*

FIG.1C



	51					100
FGF4	AELERRWESL	VALSLARLPV	AA..QPKEAA	VQSGAGDY..	...LLGIKRL	
FGF6	S...RGWGTL	LSRSRAGLAG	EI.....AG	VNWESG.Y..	...LVGIKRQ	
FGF5	SSSRQSSSSA	MSSSSASSSP	AASLGSQGS	LEQSSFQW..	...SPSGRRT	
FGF1	.....MAEG	EITTTALTE	KFN...LPPG	.....N..	...YK...KP	
FGF2	.....MAAG	SITTLPALPE	DGGSGAFPPG	.....H..	...FK...DP	
FGF9	FGNVPVLPVD	SPVLLSDHLG	QSEAGGLPRG	PAVTDLDH..	...LKGILRR	
FGF7	LACNDMTPEQ	M...ATNVNC	.....SSPE	RHTRSYDY..	...MEGGDIR	
KGF2	VTCQALGQDM	VSPEATNSSS	SSFSSPSSAG	RHVRSYNH..	...LQ.GDVR	
FGF3	PGWPAAGPGA	.....	...RLRRDAG	GRGGVYEH..	...L.GGAPR	
FGF8	FGQSRAGKN	FTNPAPNYPE	EGSKEQRDSV	LPKVTQRHVR	EQSLVTDOLS	

FIG. 2A



001 002 003 004 005 006 007 008 009 010 011 012 013 014 015 016 017 018 019 020 021 022 023 024 025 026 027 028 029 030 031 032 033 034 035 036 037 038 039 040 041 042 043 044 045 046 047 048 049 050 051 052 053 054 055 056 057 058 059 060 061 062 063 064 065 066 067 068 069 070 071 072 073 074 075 076 077 078 079 080 081 082 083 084 085 086 087 088 089 090 091 092 093 094 095 096 097 098 099 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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MATCH WITH FIG. 2A

	101		150
FGF4	RRL.....YC	NVGIGFHLQA	LPDGRIGGAH ADT.RDSLLE LSPVERGV.V
FGF6	RRL.....YC	NVGIGFHLQV	LPDGRISGTH EEN.PYSLLE ISTVERGV.V
FGF5	GSL.....YC	RVGIGFHLQI	YPDGKVNGSH EAN.MLSVLE IFAVSQGI.V
FGF1	KLL.....YC	SNG.GHFLRI	LPDGTVDGTR DRSDQHIQLQ LSAESVGE.V
FGF2	KRL.....YC	KNG.GFFLRI	HPDGRVDGVR EKSDPHIKLQ LQAEERGV.V
FGF9	RQL.....YC	R.T.GFHLEI	FPNGTIQGTR KDHSRFGILE FISIAVGL.V
FGF7	VRR.....LF	CRT.QWYLRI	DKRGKVKGTO EMKNNYNIME IRTVAVGI.V
KGF2	WRK.....LF	SFT.KYFLKI	EKNGKVSGTK KENCPSYILE ITSVEIGV.V
FGF3	RRK.....LY	CAT.KYHLQL	HPSGRVNGSL .ENSAYSILE ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA EDGDPFAKLI VETDTFGSRV

	151		200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLY	A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC LFLERLEENH YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC VFREQFEENW YNTYSSNLYK
FGF7	AIKGVSESEFY	LAMNKEGKLY	A.KKECNEDC NFKELILENH YNTYAS....
KGF2	AVKAINSNIYY	LAMNKKGKLY	G.SKEFNNDK KLKERIEENG YNTYAS....
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC EFVERIHGELG YNTYASRLYR
FGF8	RVRGAETGLY	ICMNNKGKLY	AKSNGKGKDC VFTEIVLENN YTALQNAKY.

MATCH WITH FIG. 2C

FIG. 2B



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MATCH WITH FIG. 2B

	201	250
FGF4	..... GM..... FI	ALSKNGKTKK G..NRVSPTM KVTHFLPRL.
FGF6	..... GT..... YI	ALSKYGRVKR G..SKVSPIM TVTHFLPRI.
FGF5	..... TEKTGREWYV	ALNKRKGAKR GCSPRVKPQH ISTHFLPRFK
FGF1	..... ..AEKNWFV	GLKKNNGSCKR G..PRTHYGQ KAILFLPLPV
FGF2	..... ..T..SWYV	ALKRTGQYKL G..SKTGPGQ KAILFLPMSA
FGF9	HV..... ..DTGRRYYV	ALNKDGTPRE G..TRTKRHQ KFTHFLPRPV
FGF7	..... AKW THNGGEM.FV	ALNQKGIPVR G..KKTKEQ KTAHFLPMAI
KGF2	..... FNW QHNGRQM.YV	ALNGKGAPRR G..QKTRRN TSAHFLPMVV
FGF3	TVSSTPGARR QPSAERLWYV	SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL
FGF8	..... ..EGWYM	AFTRKGRPRK G..SKTRQH REVHFMKRLP

	251	300
FGF4	.....	.....
FGF6	.....	.....
FGF5	QSEQPELSFT VTVPEKKNPP	SPIKSKIPLS APRKNTNSVK YRLKFRFG..
FGF1	SSD.....	.....
FGF2	KS.....	.....
FGF9	DPDKVPELYK DILSQS....	.....
FGF7	T.....	.....
KGF2	HS.....	.....
FGF3	DHRDHEMVRQ LQSGLP RPPG	KGVP RRRRQ KQSPDNLEPS HVQASRLGSQ
FGF8	RGHHTTEQSL RFEFLNYPPF	TRSLRGSQRT WAPEPR....

MATCH WITH FIG. 2D

FIG. 2C

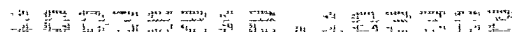


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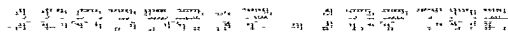
MATCH WITH FIG. 2C

	301
FGF4	.....
FGF6	.....
FGF5	.....
FGF1	.....
FGF2	.....
FGF9	.....
FGF7	.....
KGF2	.....
FGF3	LEASAH
FGF8	.....

FIG.2D

[illegible][illegible][illegible]





**FIG. 3B**



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CCCAGGGGCT TAACTGAGC AATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTAATAAGT TTAACCTTTG GAAATGCTGG CGTTCGTGA	2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTCCC	3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTCATC ATACTTTGCT TCCAAGTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTGTG GTTGAATCT GGATGTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAAGTAGGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA	4036

FIG.3C



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ATGGAATAG AATTCTGGTC CCTTTTGCAA CTAAGTGA AAAAAAAAAAG CAGTTTCAGC 4096  
CCTGAATGTT GTAGATTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156  
TTCGCCCTAT AGTGAGTCGT A 4177

FIG.3D



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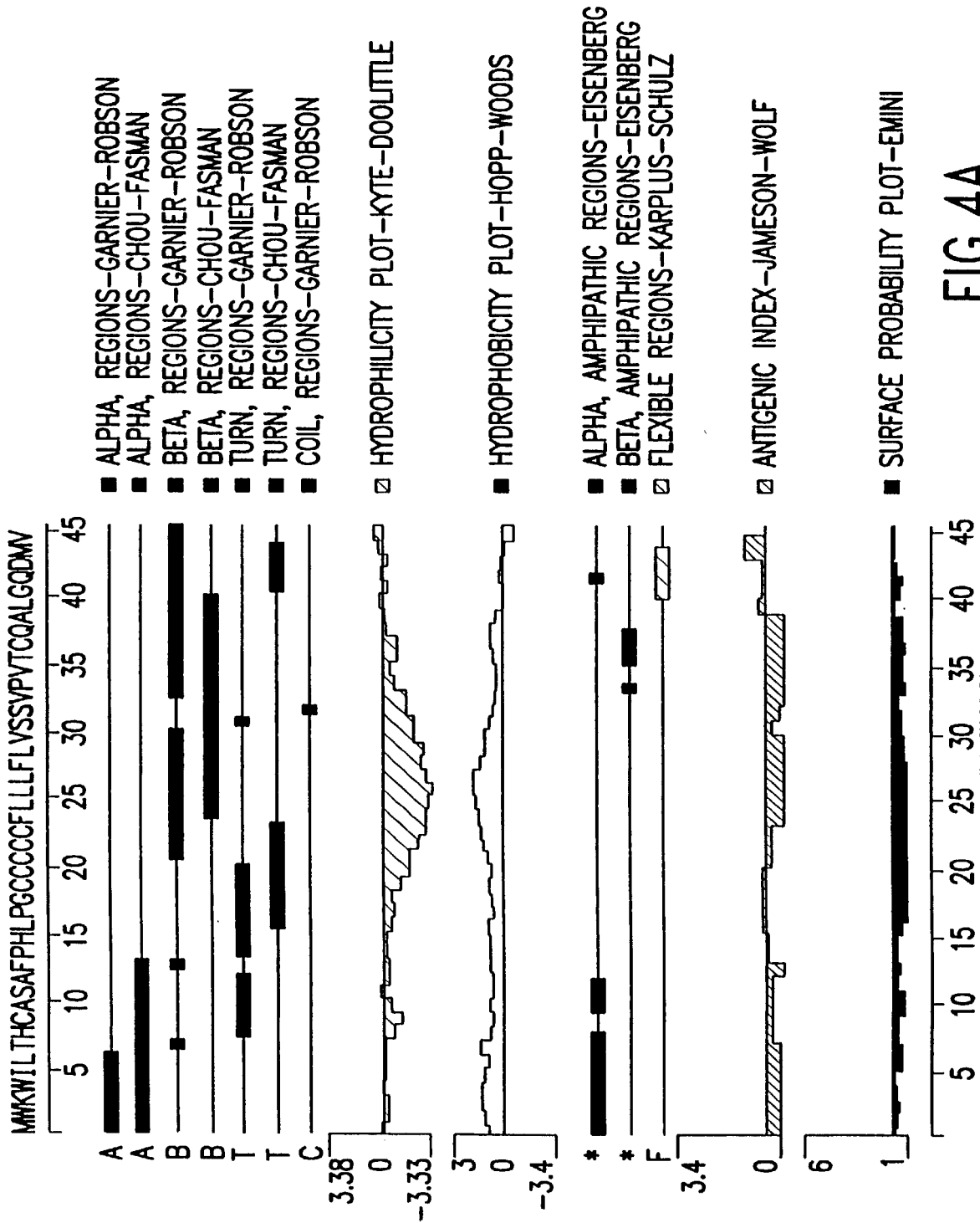
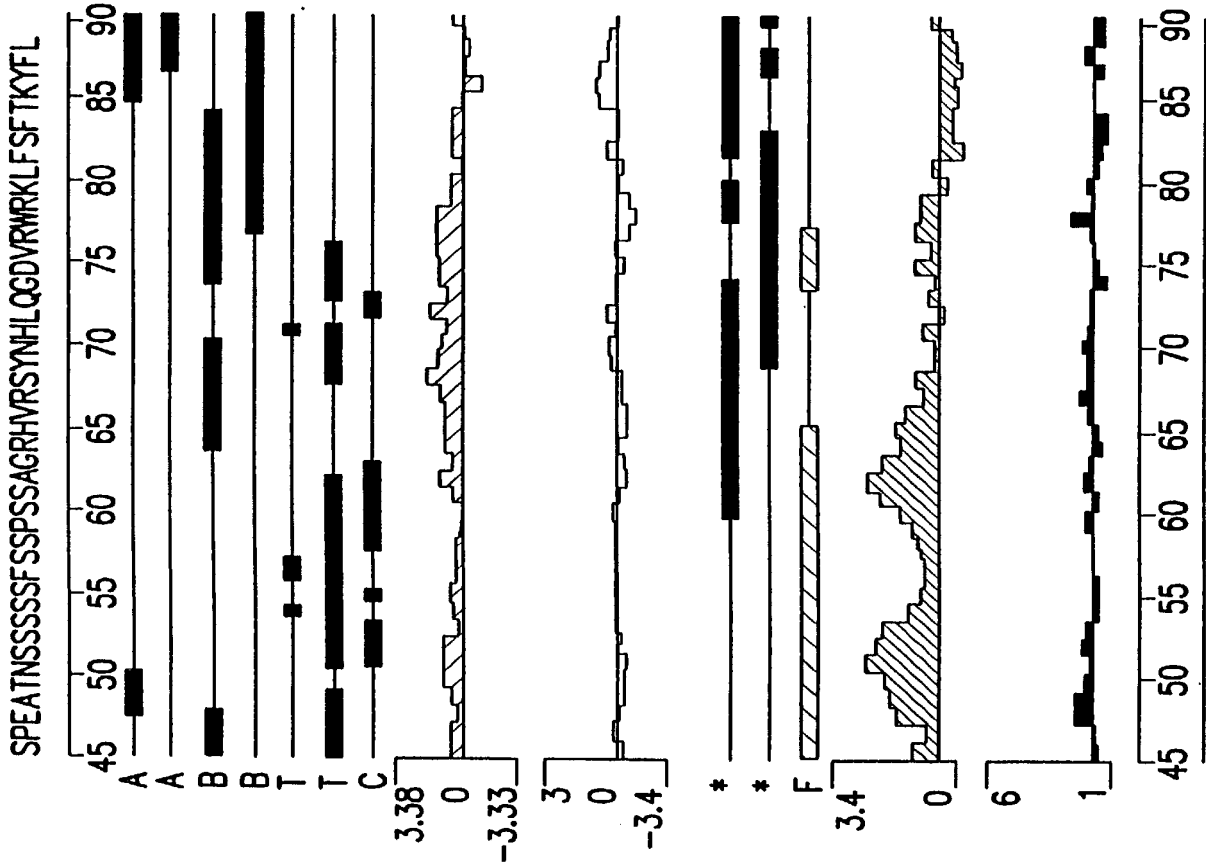


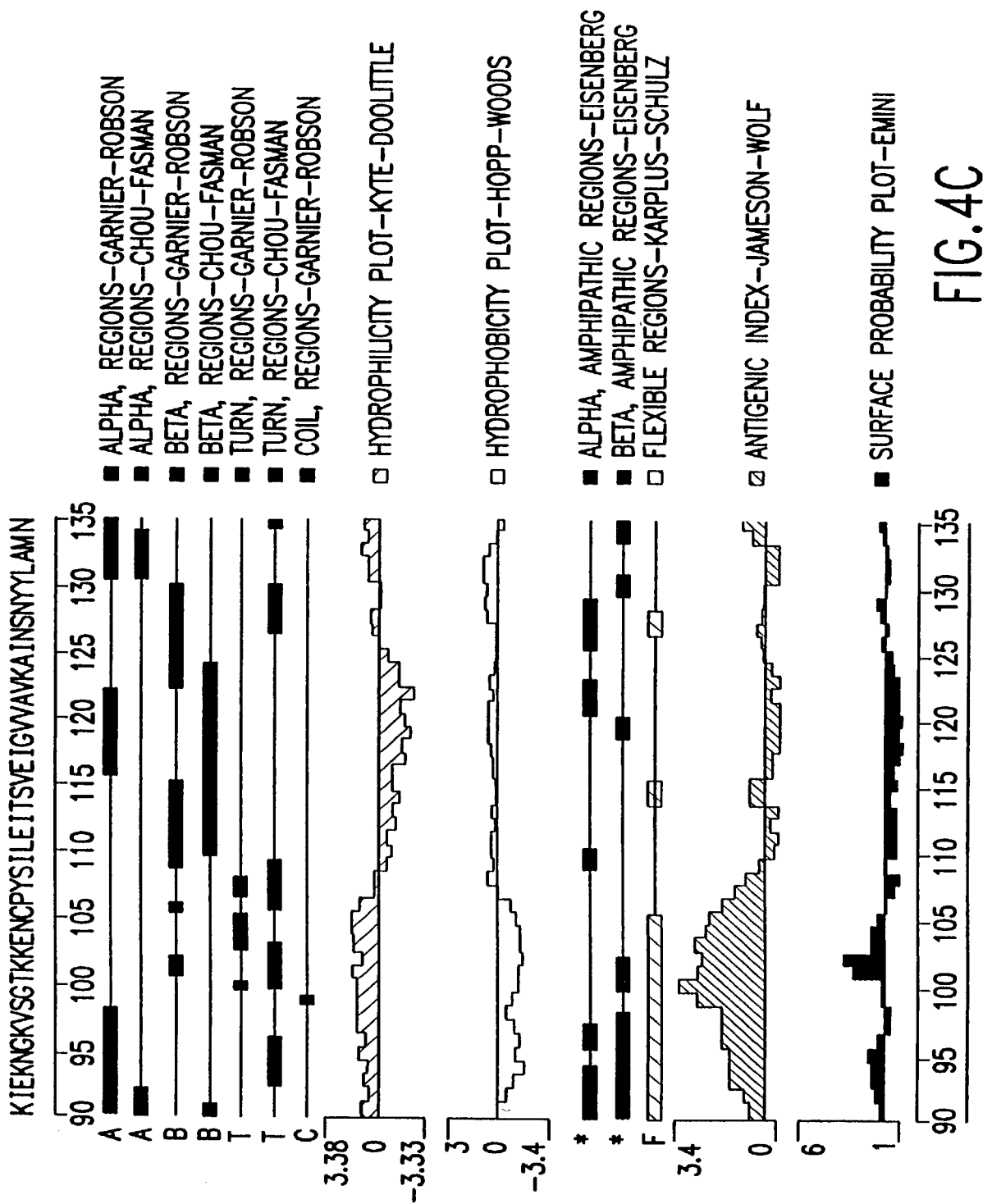
FIG.4A



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FIG.4B

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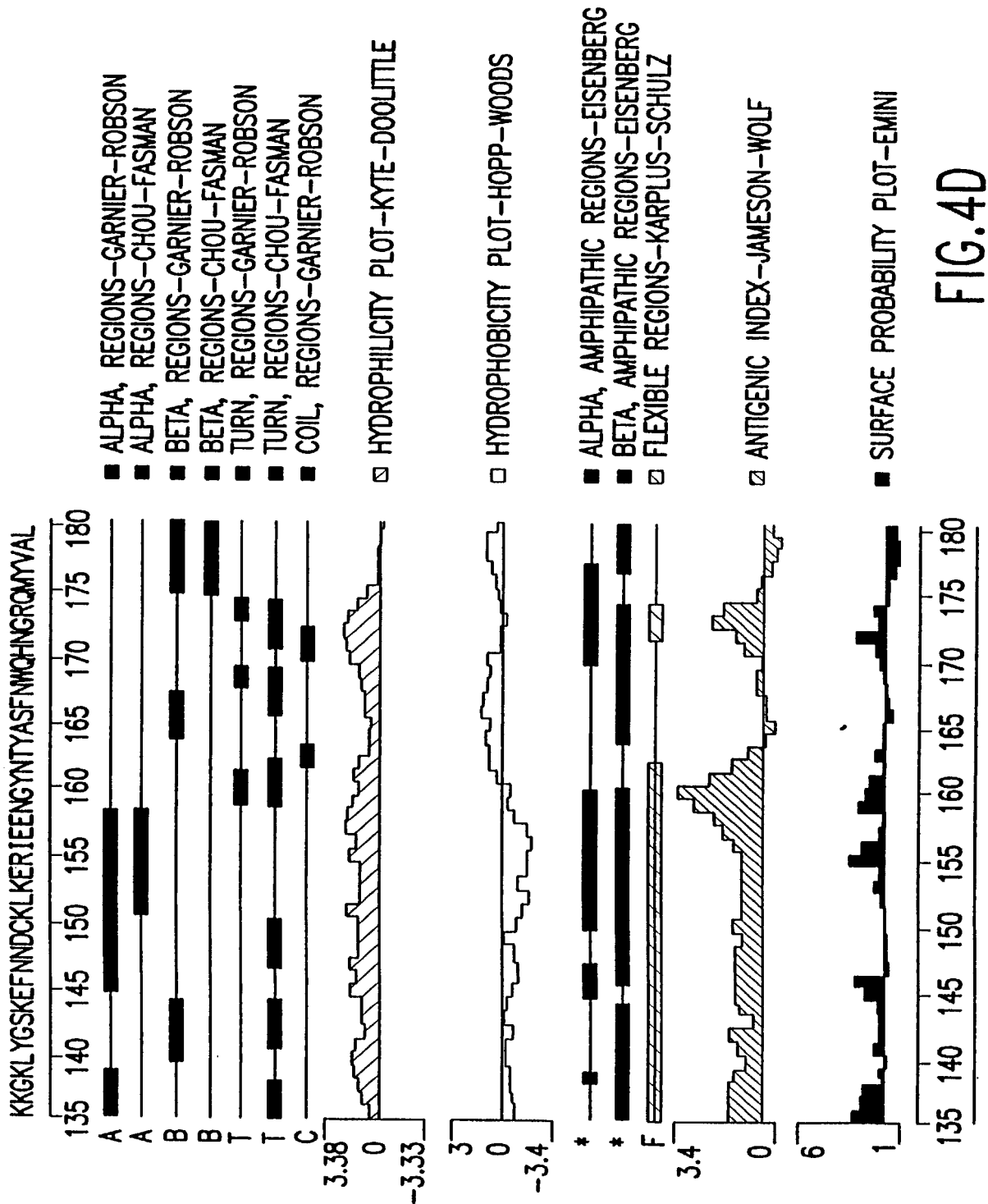
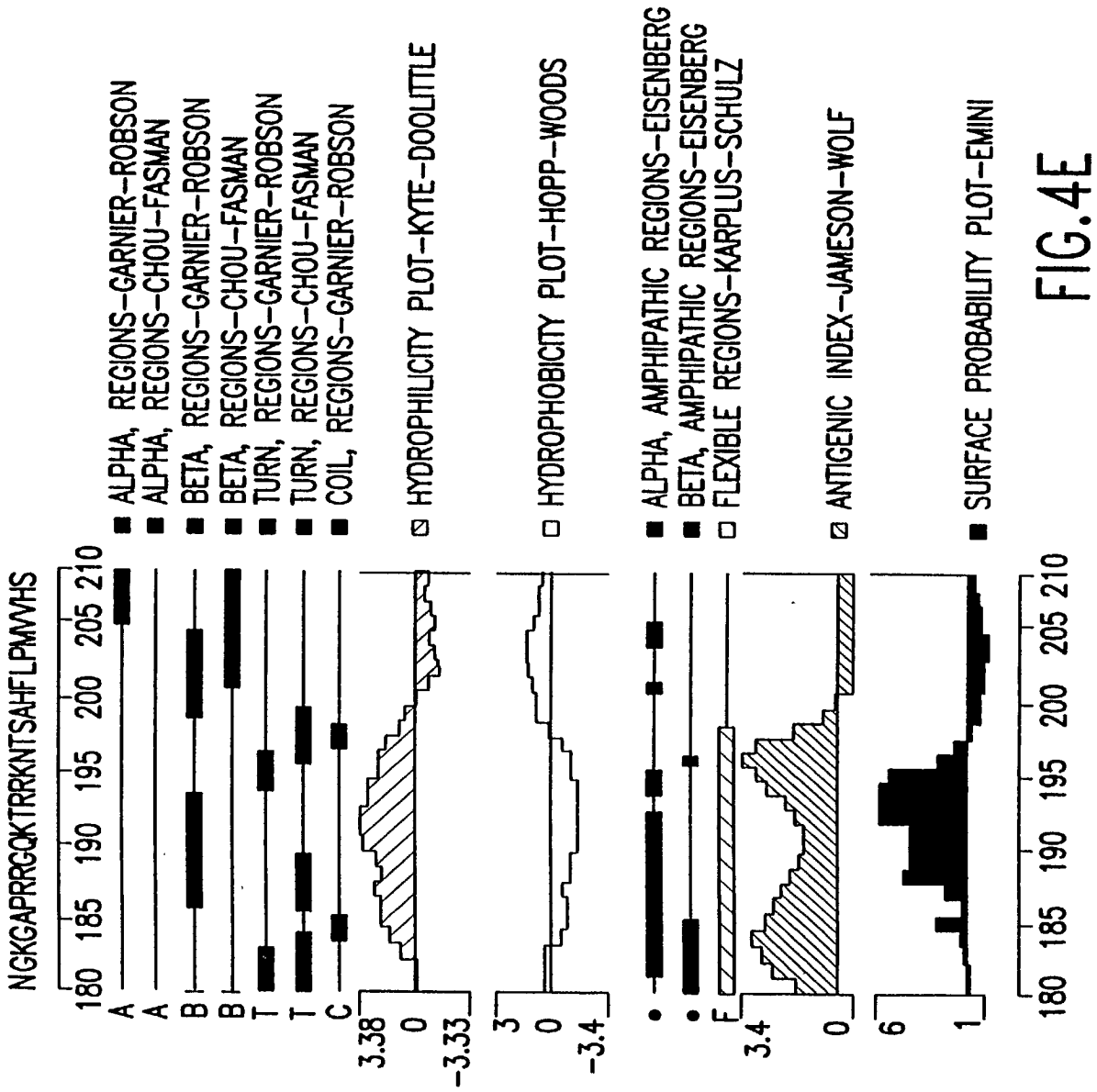


FIG. 4D is a schematic diagram of a protein structure, showing a sequence of amino acids and their corresponding properties. The diagram is divided into several sections, each representing a different type of protein region or property. The sections are labeled as follows: ALPHA, REGIONS-GARNIER-ROBSON; ALPHA, REGIONS-CHOU-FASMAN; BETA, REGIONS-GARNIER-ROBSON; BETA, REGIONS-CHOU-FASMAN; TURN, REGIONS-GARNIER-ROBSON; TURN, REGIONS-CHOU-FASMAN; COIL, REGIONS-GARNIER-ROBSON; HYDROPHILICITY PLOT-KYTE-DOOLITTLE; HYDROPHOBICITY PLOT-HOPP-WOODS; ALPHA, AMPHIPATHIC REGIONS-EISENBERG; BETA, AMPHIPATHIC REGIONS-EISENBERG; FLEXIBLE REGIONS-KARPLUS-SCHULZ; ANTIGENIC INDEX-JAMESON-WOLF; SURFACE PROBABILITY PLOT-EMINI. The diagram shows a sequence of amino acids from 135 to 180, with various regions and properties indicated by different symbols and colors. The regions are represented by solid black bars, while the properties are represented by different patterns of lines and dots. The diagram is a schematic representation of a protein structure, showing the sequence of amino acids and their corresponding properties.



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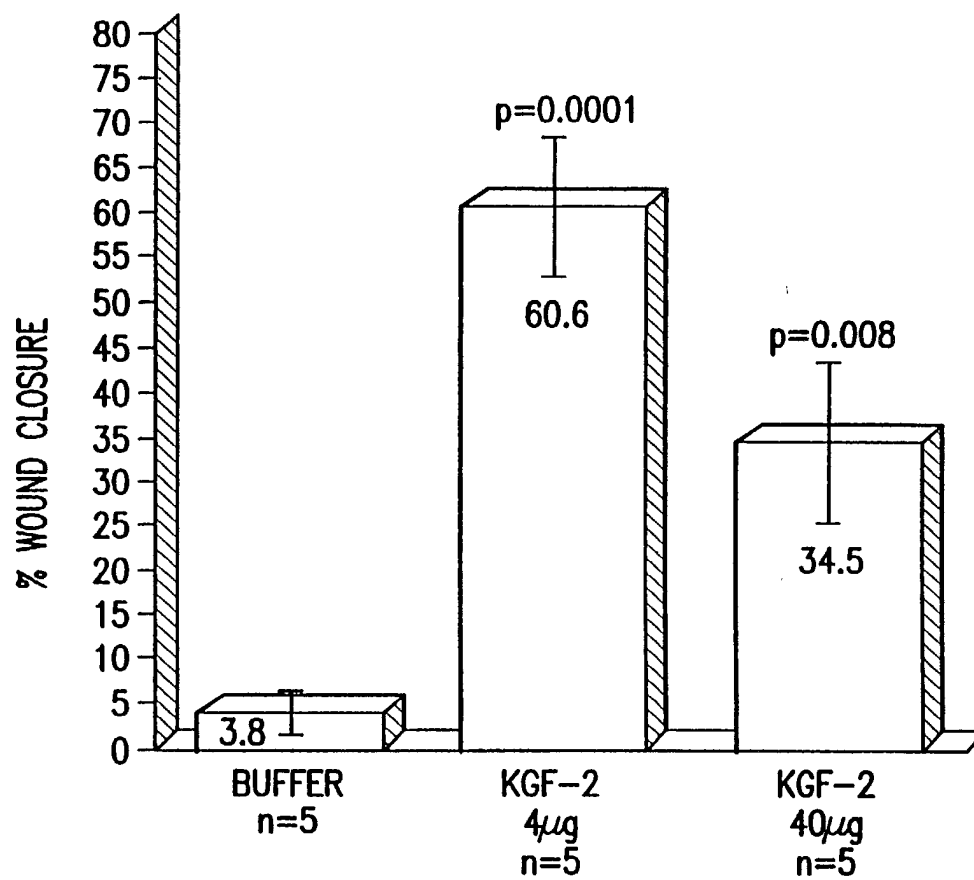


FIG.5



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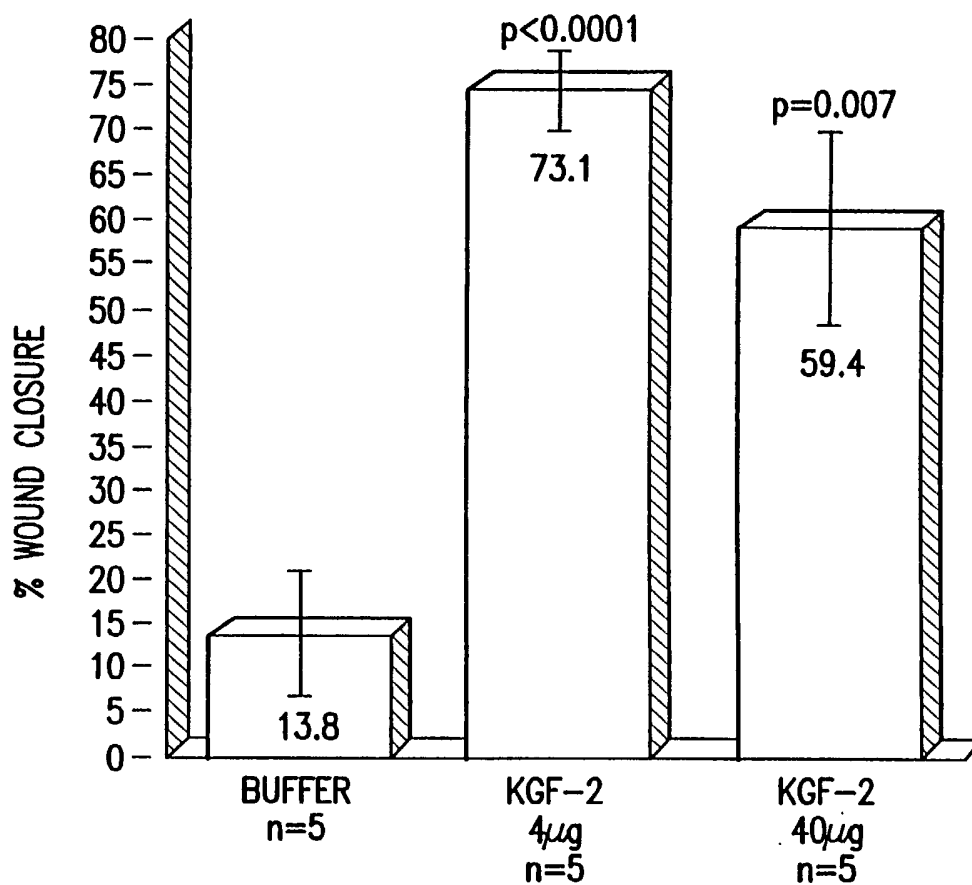


FIG.6



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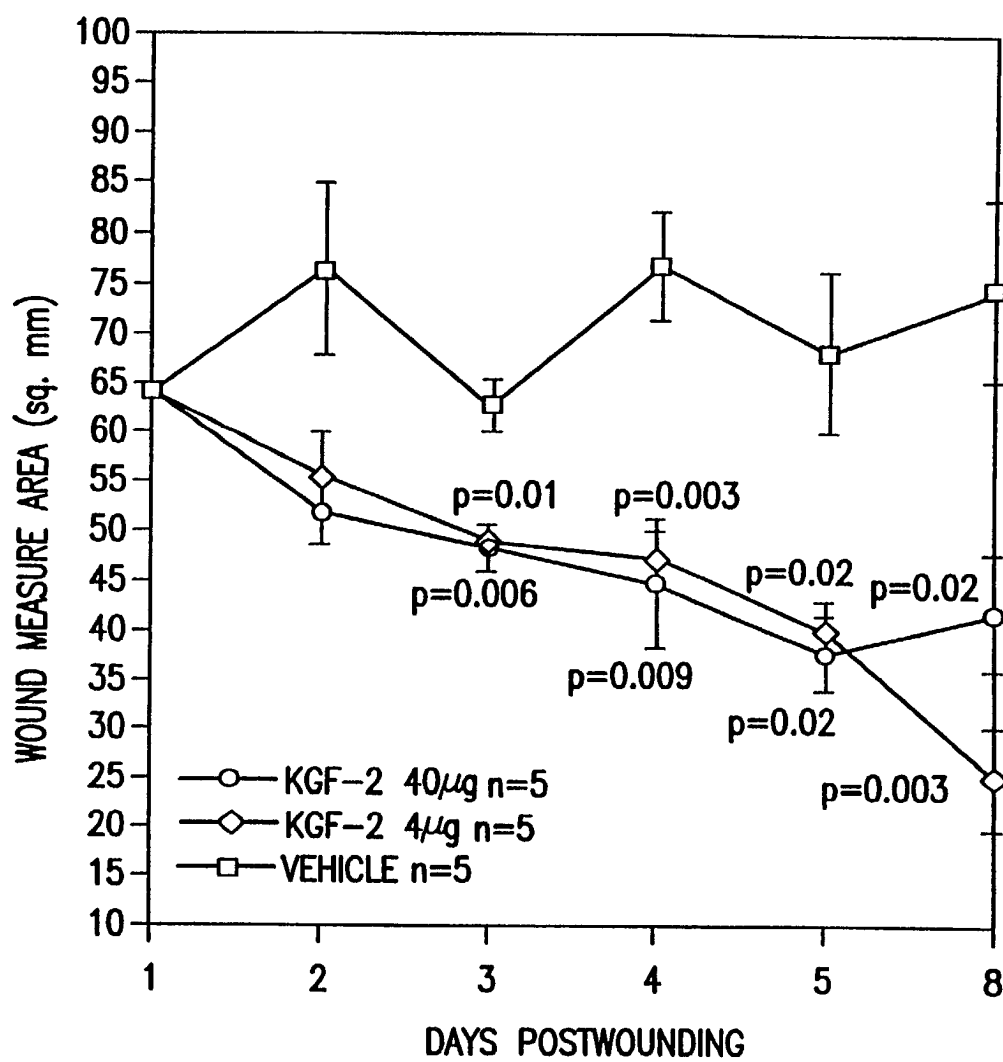


FIG.7



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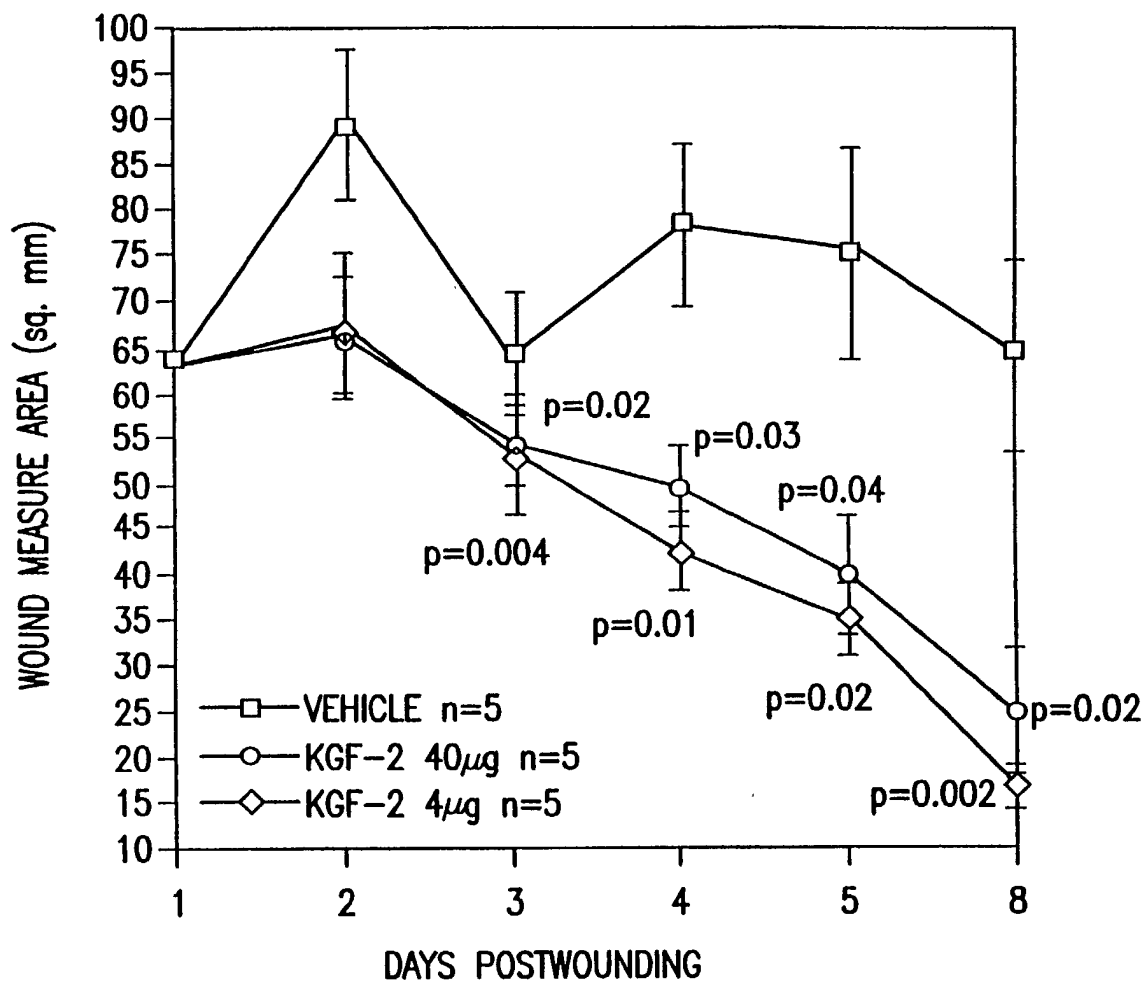
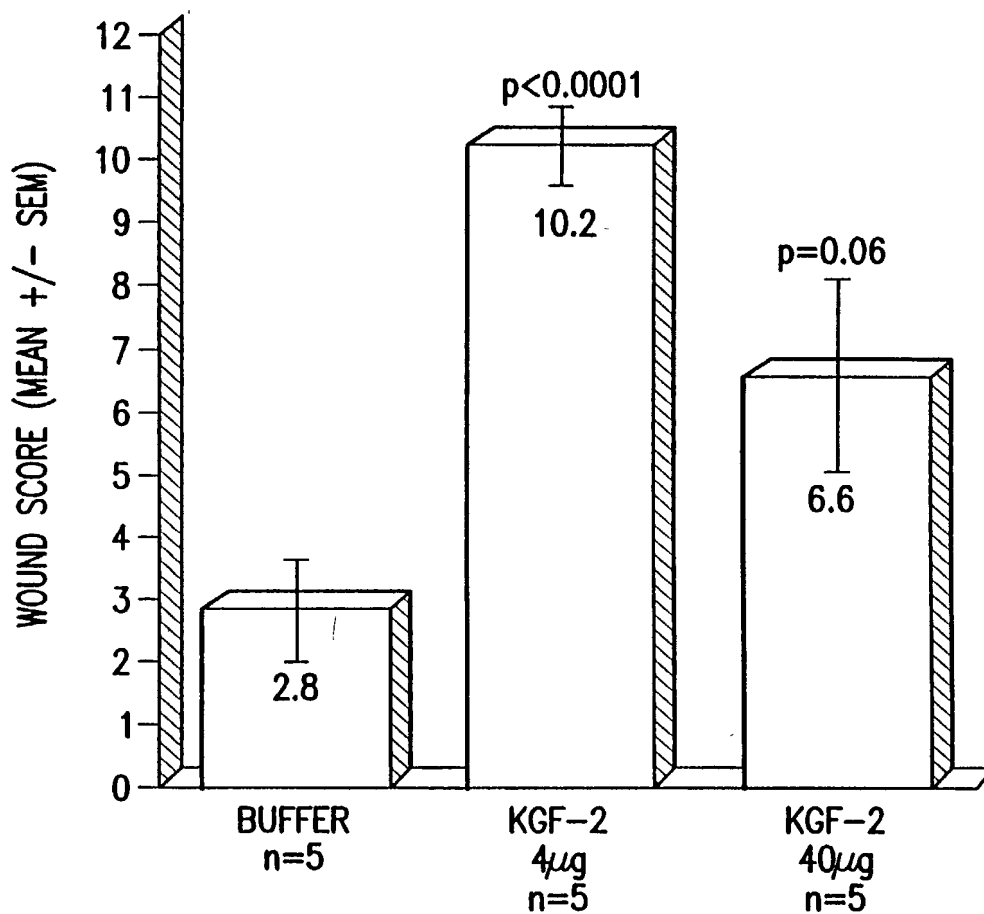


FIG.8



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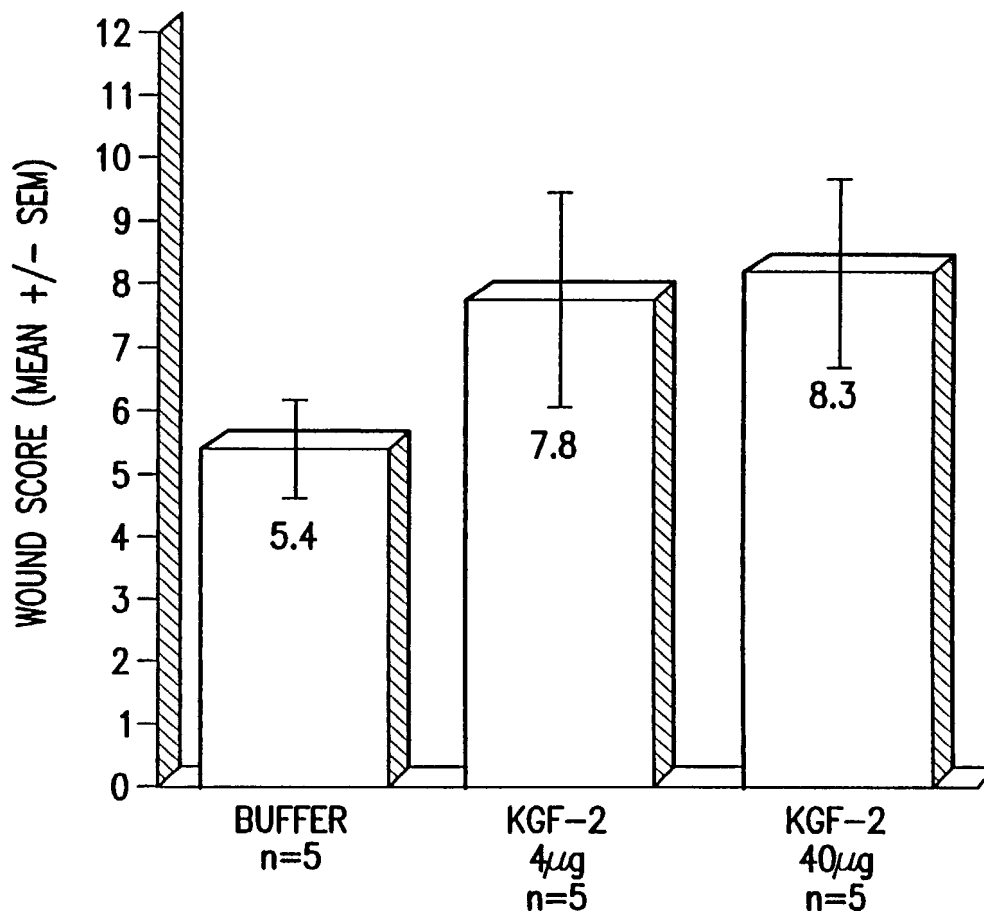


1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



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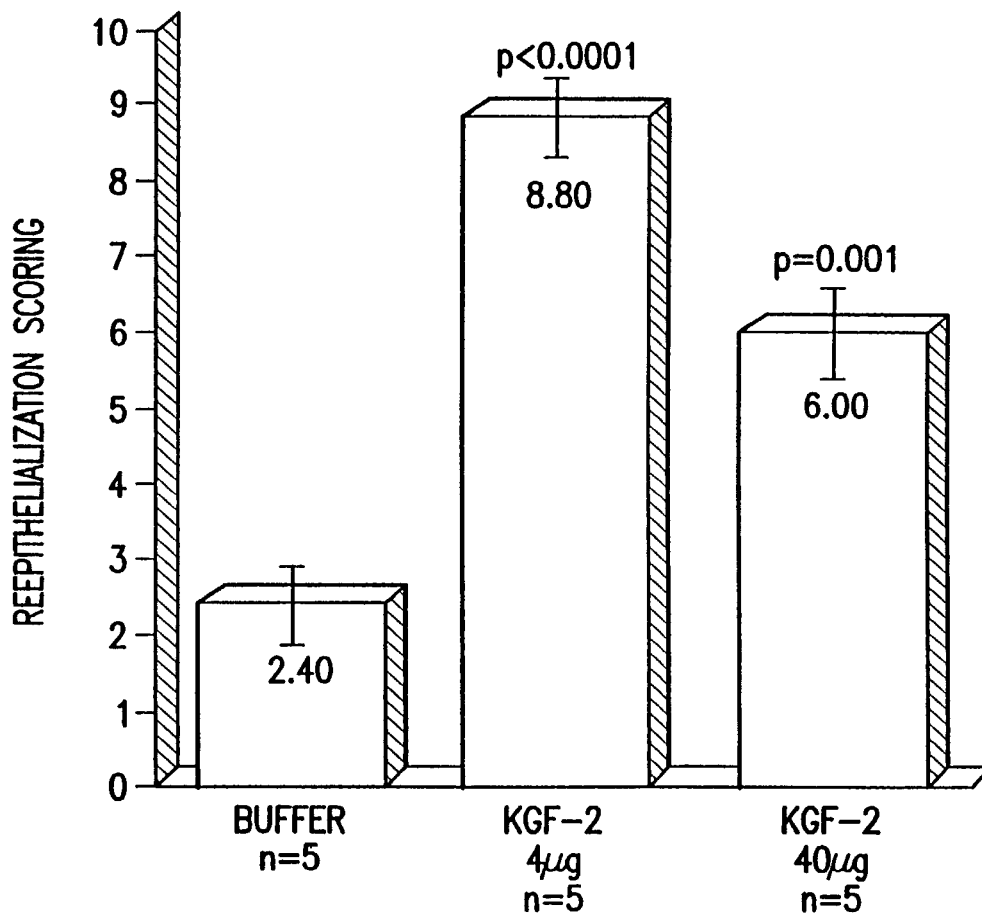


1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM  
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10

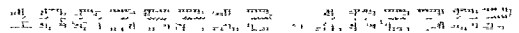


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ANTI-CYTOKERATIN IMMUNOSTAINING  
0-NO CLOSURE  
5-SLIGHT TO MODERATE CLOSURE  
10-COMPLETE CLOSURE

FIG.11



Group	n	Mean Score	p-value
BUFFER	5	3.0	
KGF-2 4µg	5	8.2	0.006
KGF-2 40µg	5	7.4	0.01

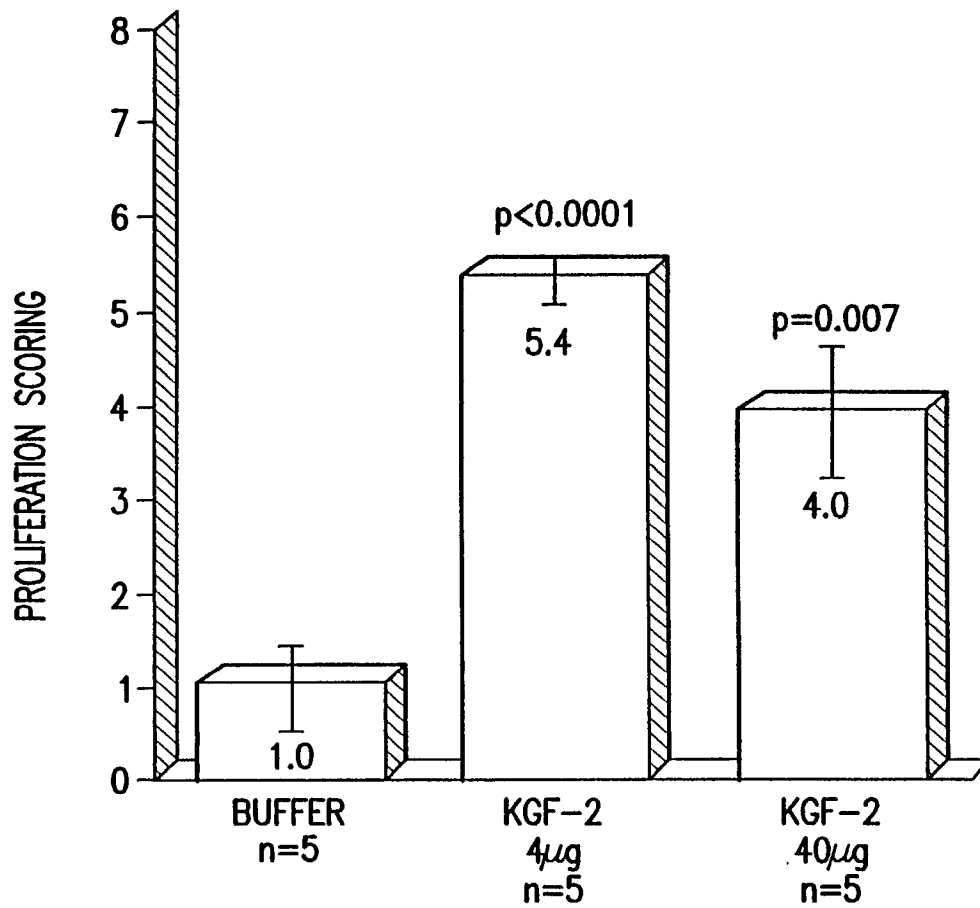
FIG.12





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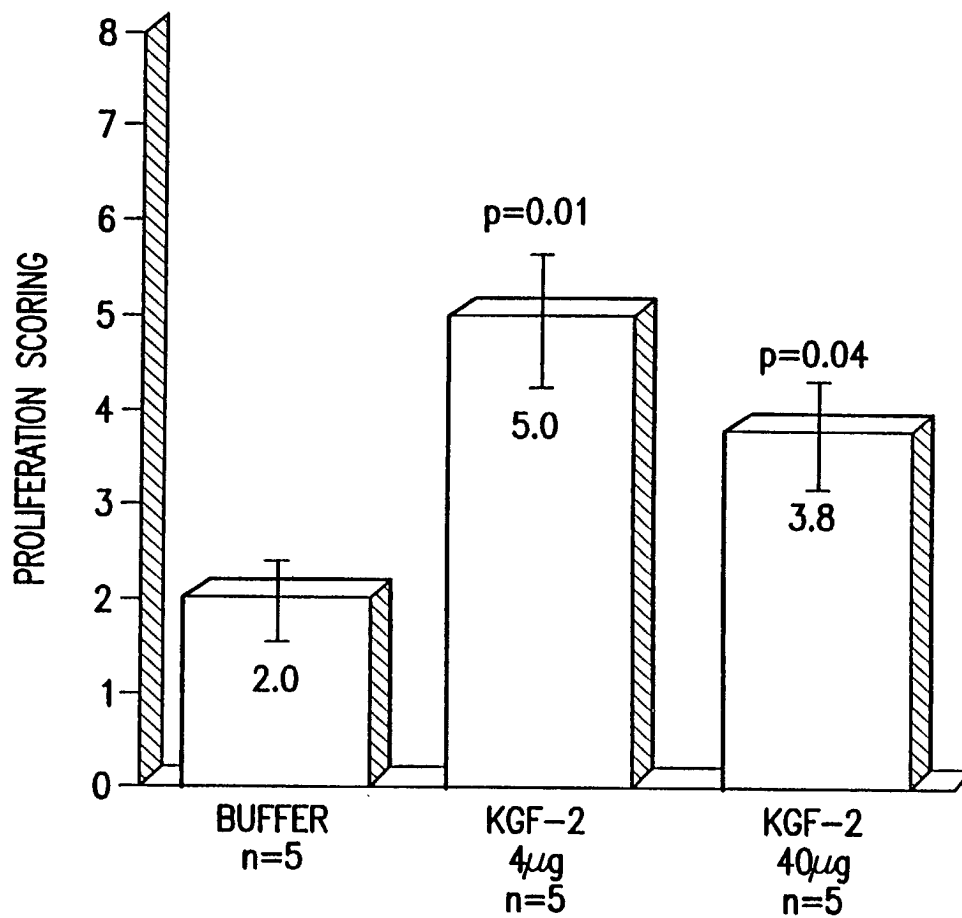
PCNA SCORING  
0-2 SLIGHT PROLIFERATION  
3-5 MODERATE PROLIFERATION  
6-8 INTENSE PROLIFERATION

FIG.13



Figure 14: Bar chart showing PCNA Scoring for three groups: BUFFER, KGF-2 4μg, and KGF-2 40μg. The y-axis represents Proliferation Scoring from 0 to 8. The x-axis shows the groups. The BUFFER group has a mean score of 2.0. The KGF-2 4μg group has a mean score of 5.0 with a p-value of 0.01 compared to the BUFFER group. The KGF-2 40μg group has a mean score of 3.8 with a p-value of 0.04 compared to the BUFFER group. Error bars represent standard deviation.

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PCNA SCORING  
0-2 SLIGHT PROLIFERATION  
3-5 MODERATE PROLIFERATION  
6-8 INTENSE PROLIFERATION

FIG.14



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ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC  
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCTTCTTCTTCTTCTTCCC  
CGTCTTCCGCTGGTCGTACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTT  
GTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCTGAAAATCGAAAAA  
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAAGTCCCGTACAGCATCCTG  
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAG  
CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAG  
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT  
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT  
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG  
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD  
VRWRKLFSTKYFLKIEKNGKVSGETTKENCPSILEITSVEIGVVAVKAINSN  
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI  
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15



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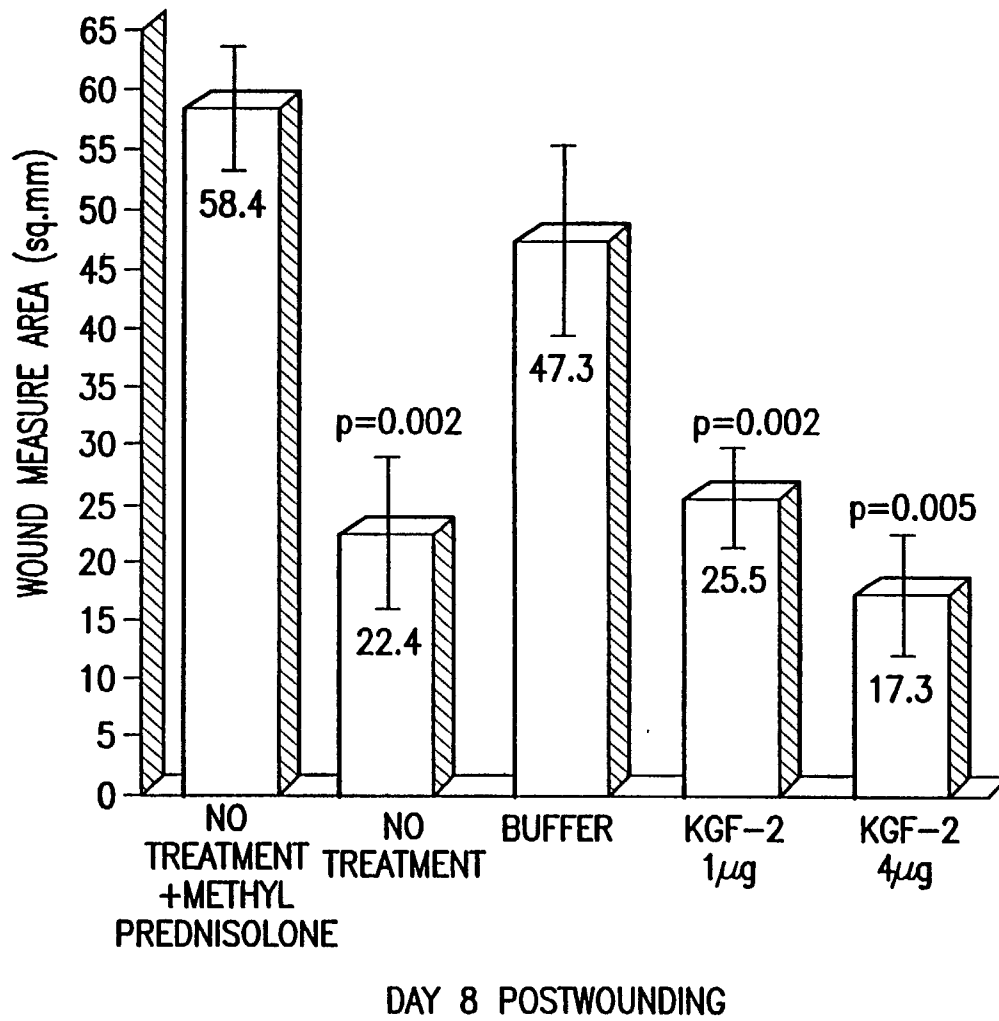
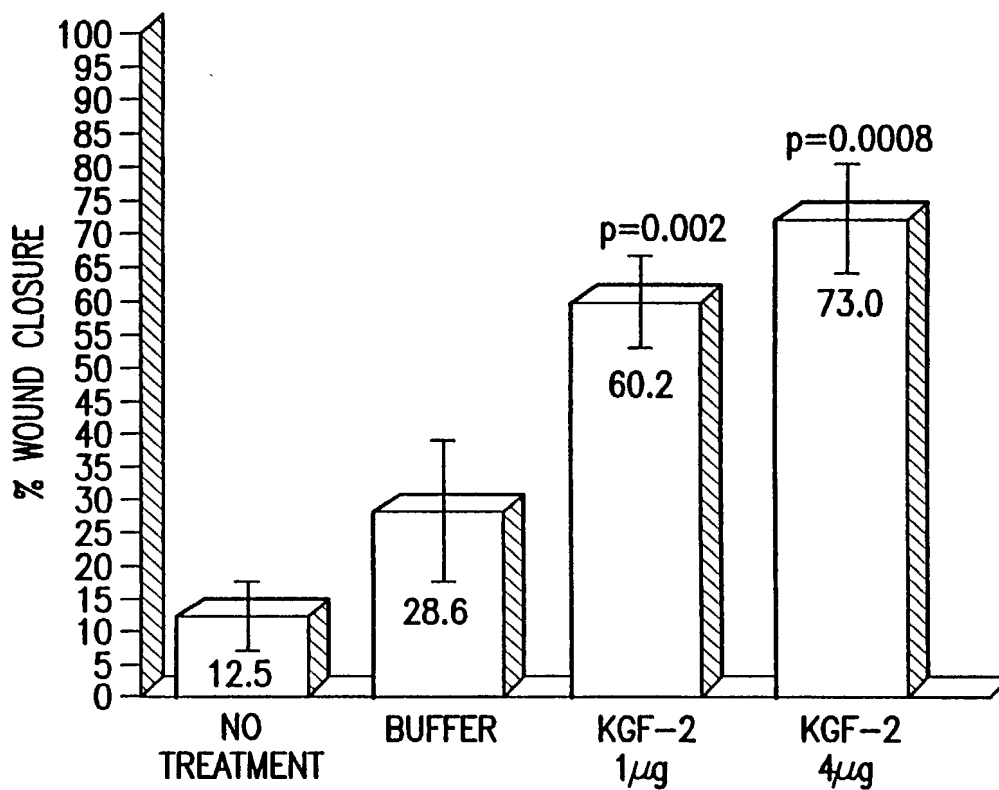


FIG.16



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GLUCOCORTICOID TREATED ANIMALS

FIG.17



From: [illegible] To: [illegible] Subject: [illegible]

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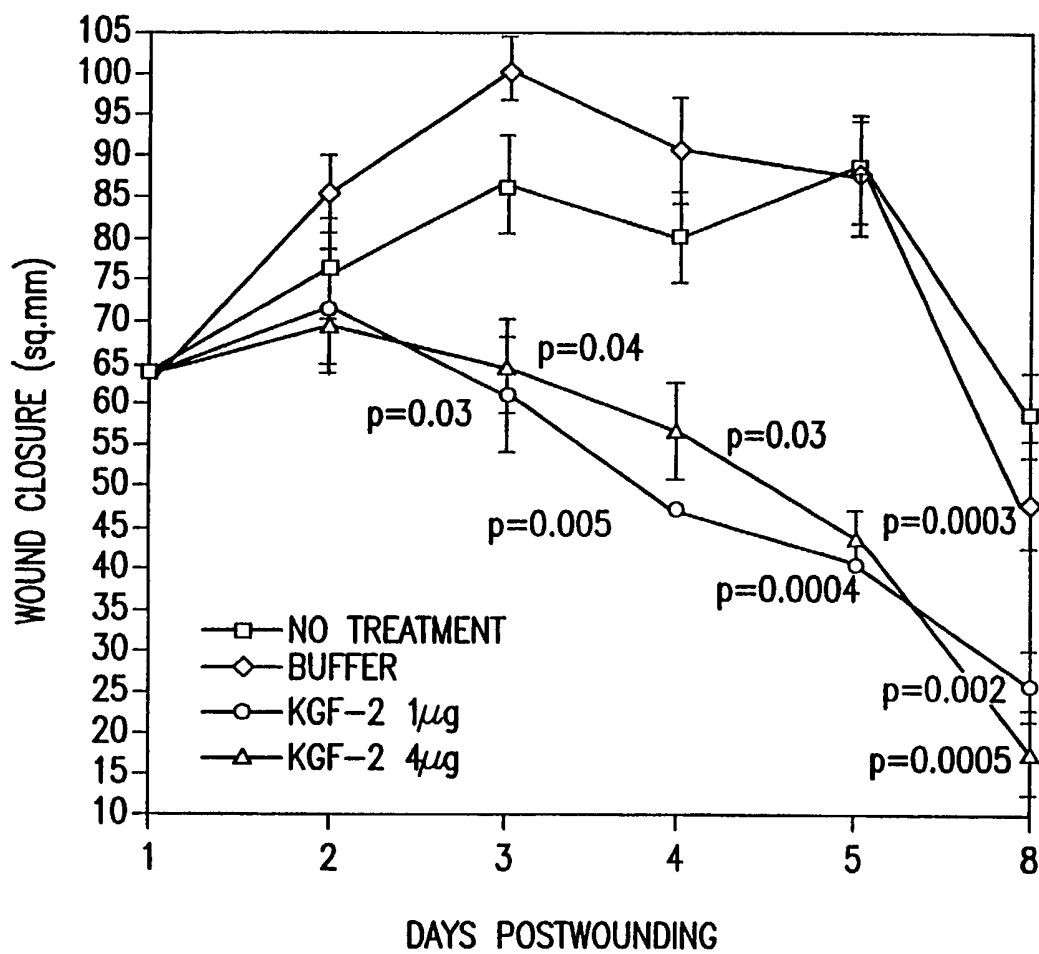


FIG.18



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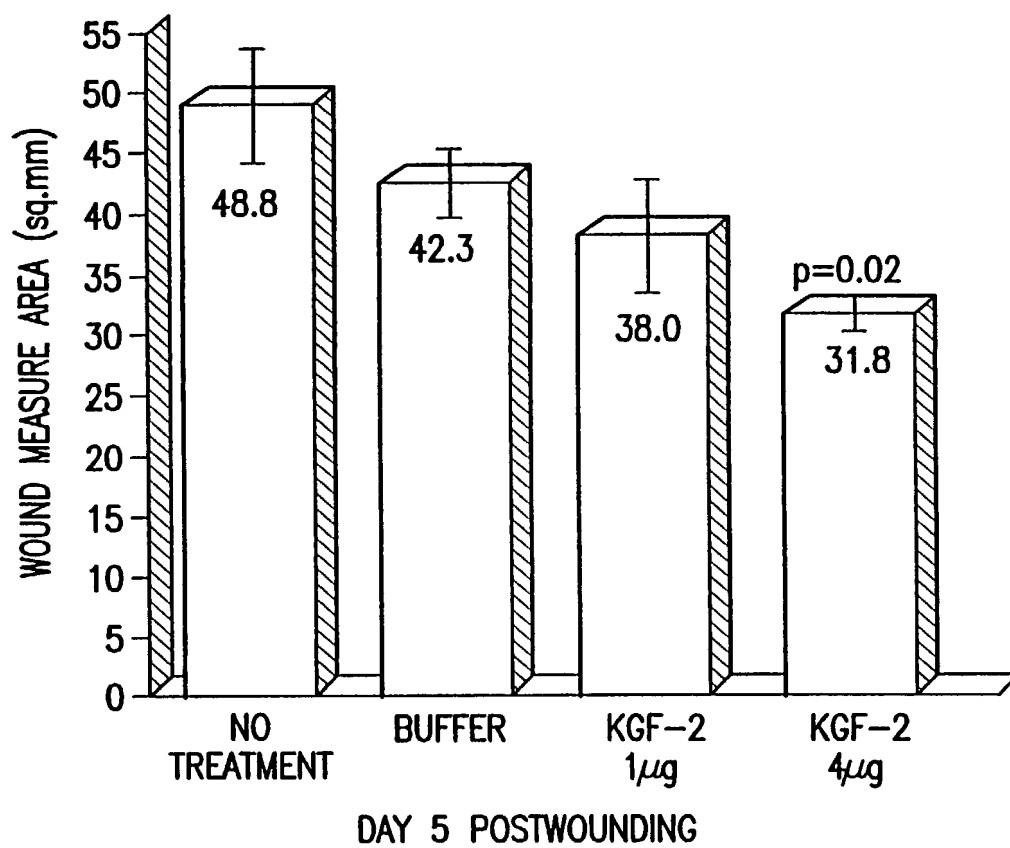
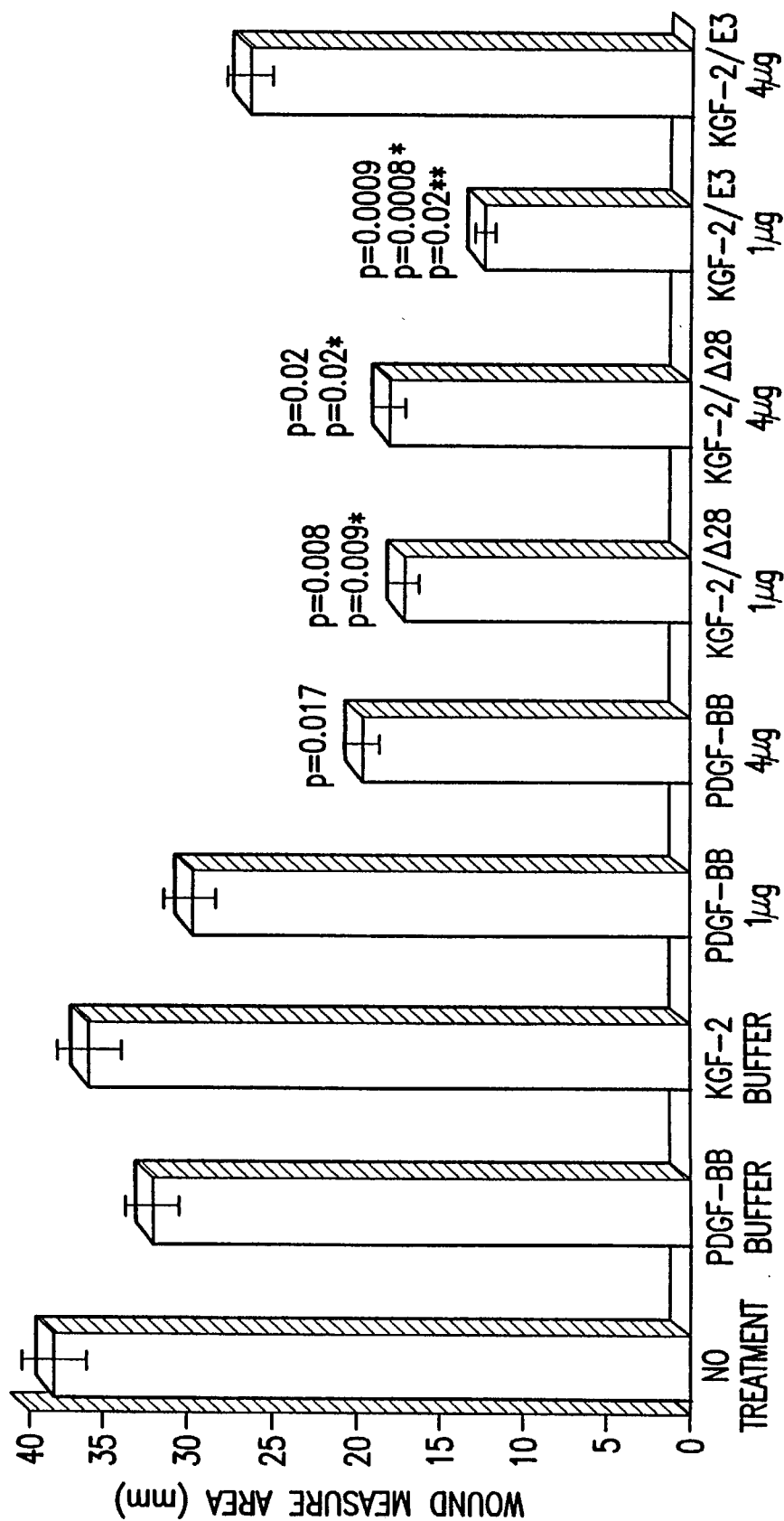


FIG.19A



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DAY 10 POSTWOUNDING

FIG.19B





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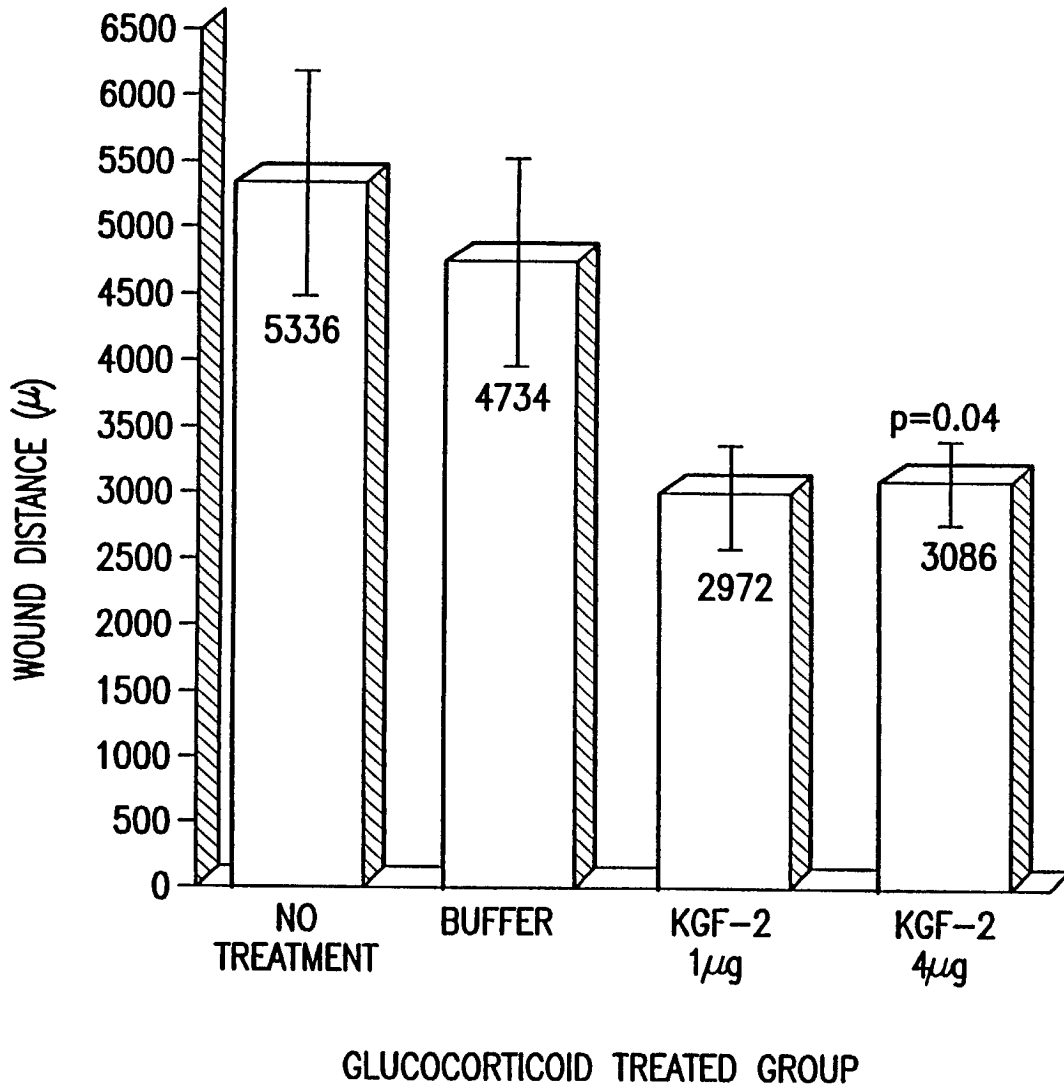


FIG.20



FIG. 21A

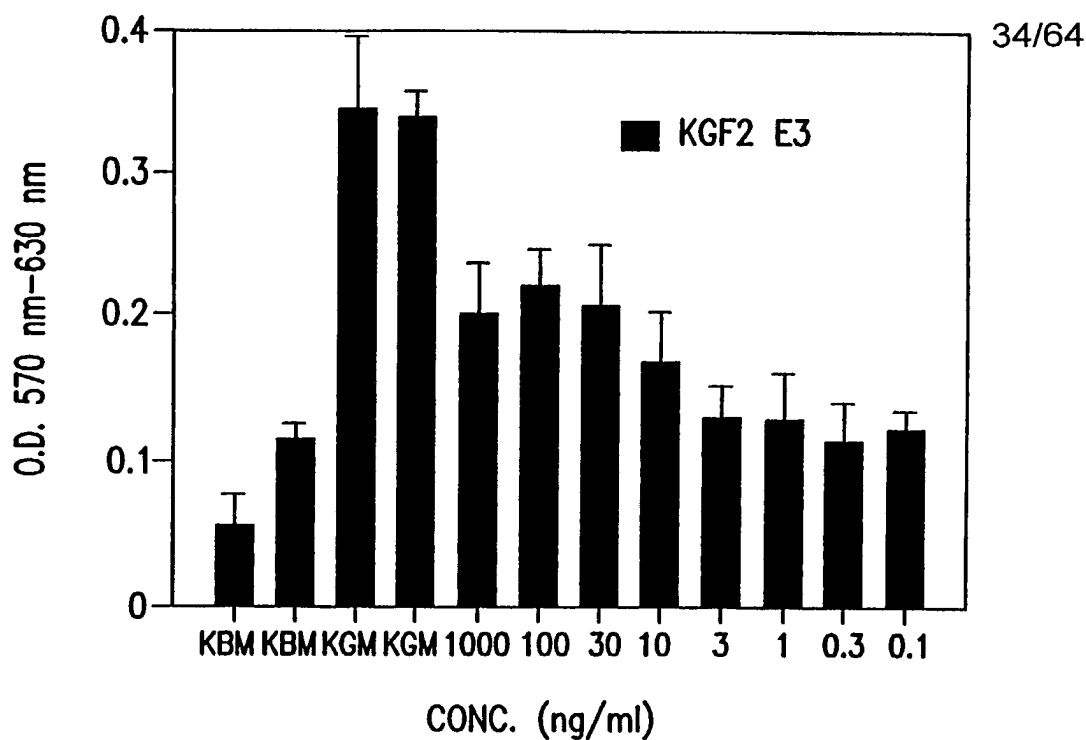


FIG.21A

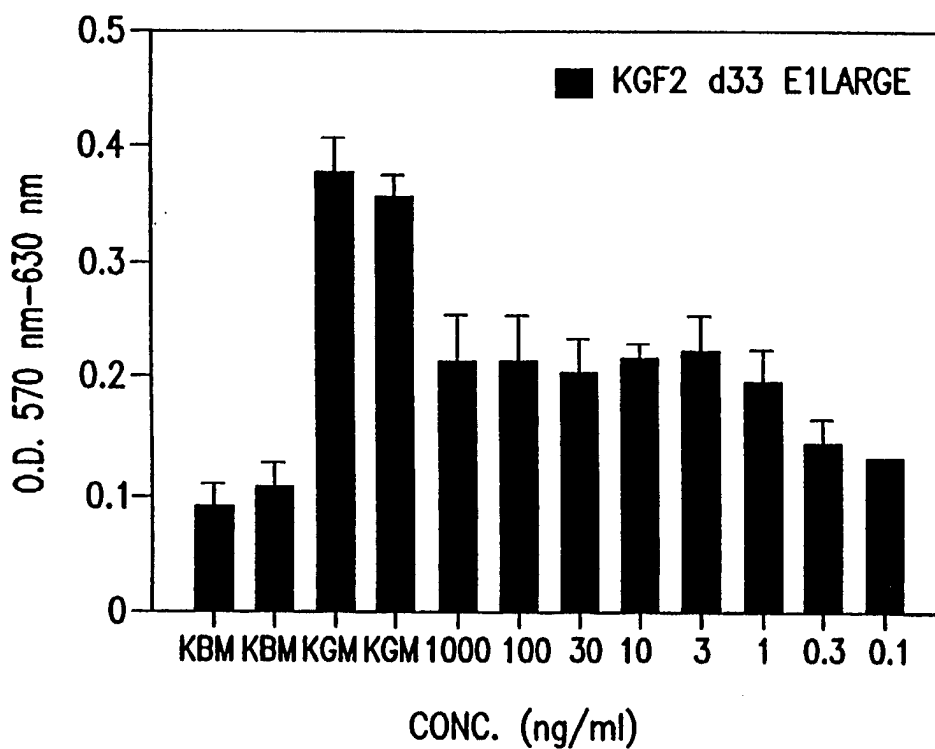


FIG.21B



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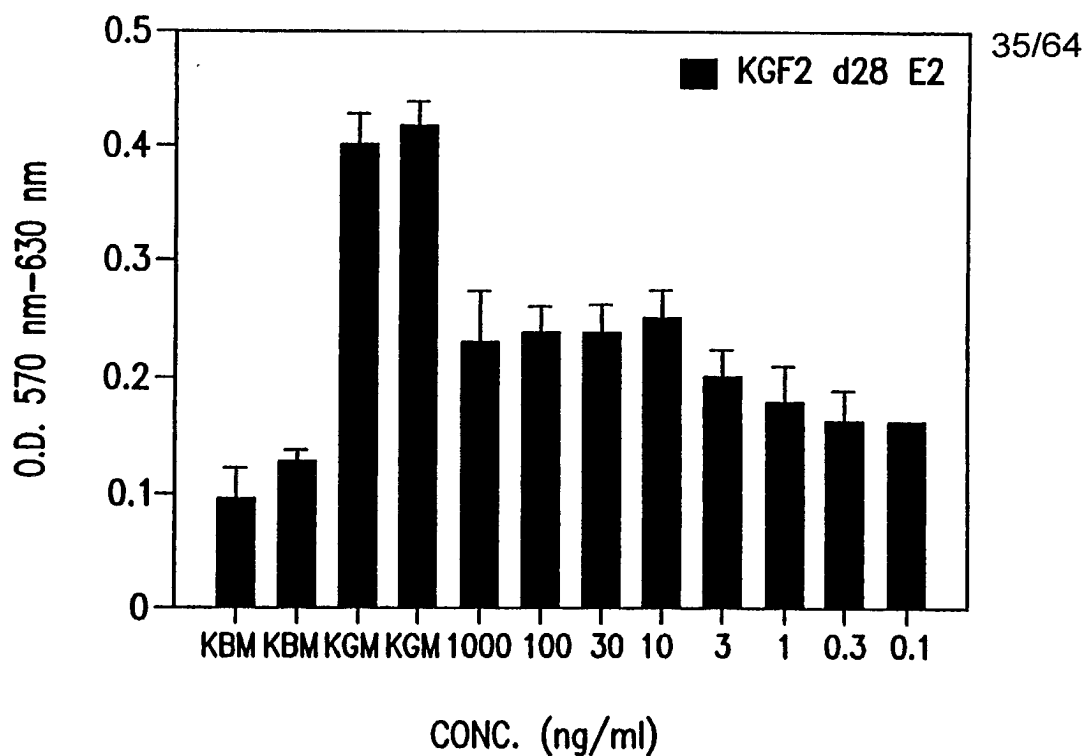


FIG.21C

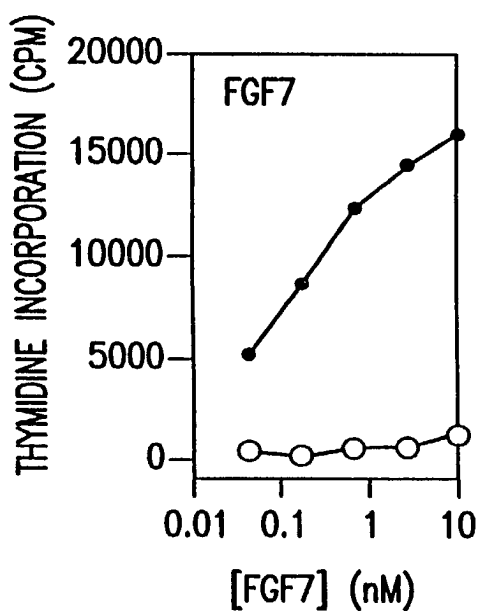


FIG.22A

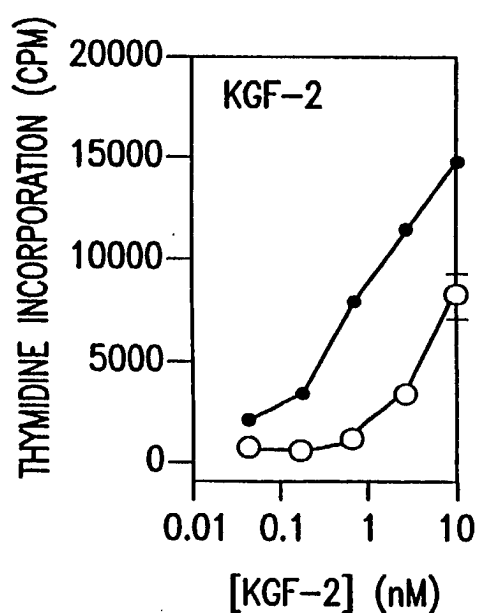


FIG.22A-1



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Page: 1 of 1  
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User: jcs8102

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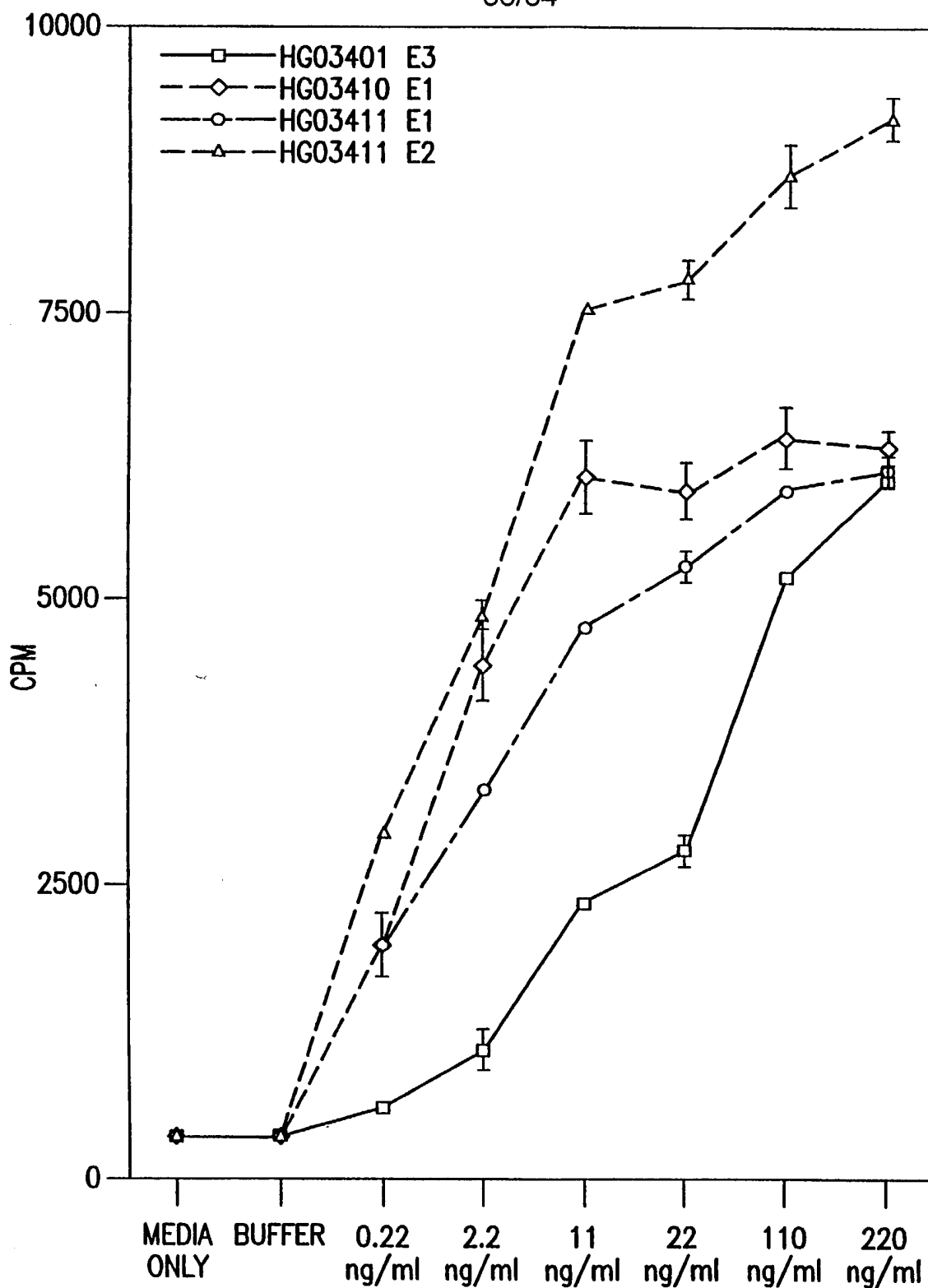


FIG.22B



FIG. 22C is a bar graph showing the results of a competition assay. The y-axis represents CPM (Counts Per Minute) and the x-axis represents the concentration of the competitor (ng/ml). The legend indicates three conditions: 3401-E3 (white bars), DELTA 28-E1 (hatched bars), and DELTA 33-E1 (black bars). The graph shows that the binding of 3401-E3 is significantly inhibited by the presence of DELTA 28-E1 and DELTA 33-E1, especially at higher concentrations (220 ng/ml and 110 ng/ml). Error bars are present on all data points.

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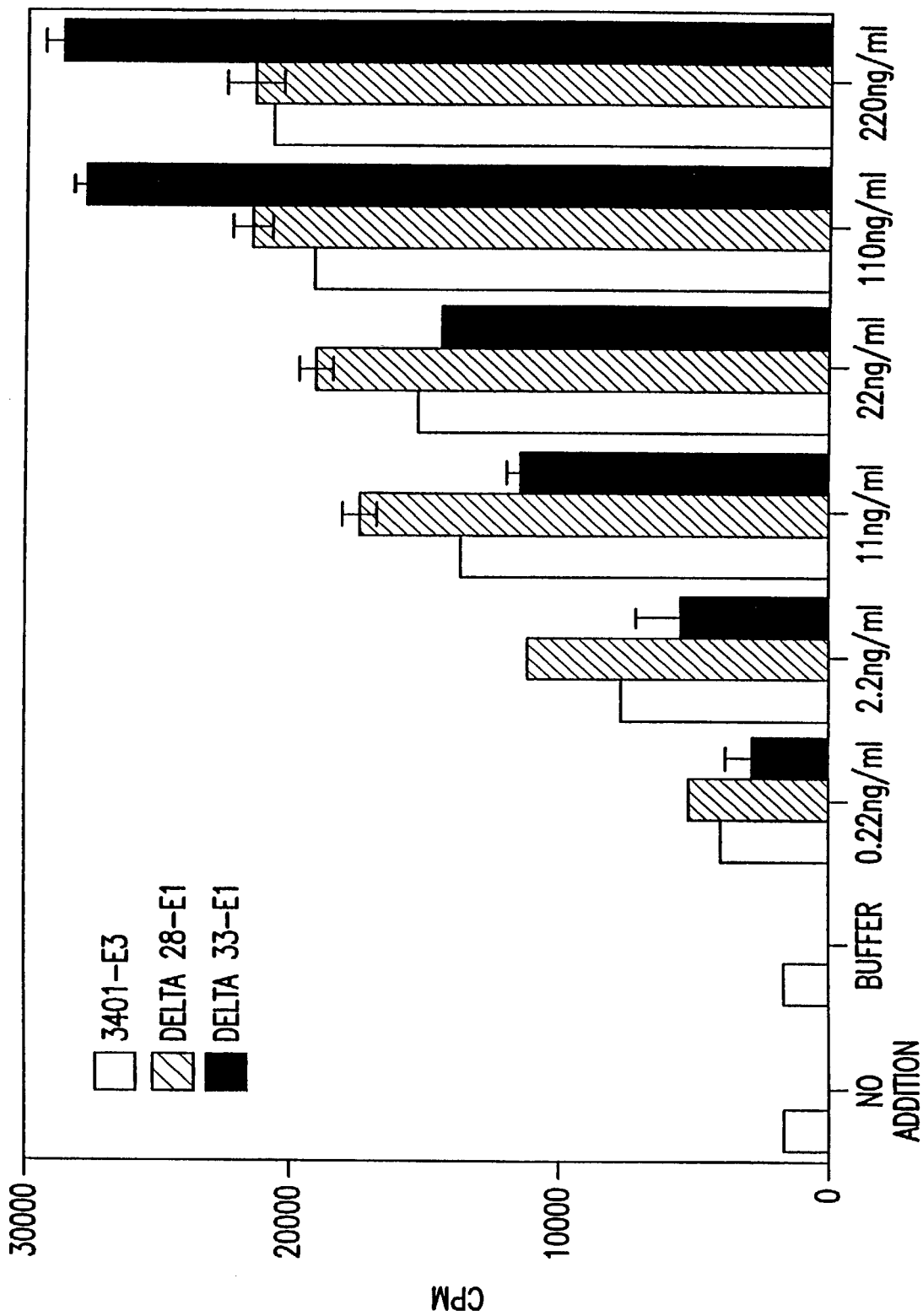


FIG.22C



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ATGTGGAATGGATACTGACCCACTGCGCTTCTGCTTCCCGCACCTGCCGGGTGCTGC 60  
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys

TGCTGCTGCTTCCTGCTGCTGTTCTGTTCCGGTTACCTGCCAGGCTCTG 120  
Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu

GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCCCG 180  
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro

ACTTCCGCTGGTCGTACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTTCGTTGGCGT 240  
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg

AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCTGGG 300  
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly

ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360  
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val

GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 420  
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu

TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480  
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly

TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCCAAATGTATGTGGCATTG 540  
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600  
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His

TTTCTTCCAATGGTGGTACACTCATAG 627  
Phe Leu Pro Met Val Val His Ser \*

FIG. 23



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ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60  
MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer

TCCTCTTTCTCTTCCCCGTCTTCGCTGGTCGTCACGTTCTTACAACCACCTGCAG 120  
SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln

GGTGACGTTTCGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180  
GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240  
AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300  
SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet

AACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360  
AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420  
ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg

CAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480  
GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525  
LysAsnThrSerAlaHisPheLeuProMetValValHisSer \*

FIG.24A



ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA 40/64  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++| 70  
TACTGAACGGTCCGTGACCCAGTTCTGTACCAAGGGCCTTCGATGGTTGTGAGGTGAGATCGAAGT  
M T C Q A L G Q D M V S P E A T N S S S S S F  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
GCAGCCCATCTAGCGCAGGTGTCAGTTGCTCTTACAACCACTTACAGGGTGATGTTGCTTGGCGCAA 140  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
CGTCGGGTAGATCGCGTCCAGCAGTCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT  
S S P S S A G R H V R S Y N H L Q G D V R W R K  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
ACTGTTCACTTTACCAAGTACTTCTGAAAATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG 210  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
TGACAAGTCGAAATGGTTCATGAAGGACTTTAGCTTTTTTTGCCATTTCAAAGACCTGGTTCTTCCTC  
L F S F T K Y F L K I E K N G K V S G T K K E  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
AACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA 280  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
TTGACGGGCATGTGCTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGGTAATTGT  
N C P Y S I L E I T S V E I G V V A V K A I N  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAA 350  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
CGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAGATACGAGTTTCTTAAATTGTTACTGACATT  
S N Y Y L A M N K K G K L Y G S K E F N N D C K  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
GCTGAAGGAGAGGATAGAGGAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTGTATTACCTCC  
L K E R I E E N G Y N T Y A S F N W Q H N G R  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
CAAATGTATGTGCATTGAATGAAAAGGAGCTCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCT 490  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
GTTTACATACACGTAACCTTACCTTTTCTCGAGGTTCTCTCCTGTCTTTGTGCTTCTTTTGTGGA  
Q M Y V A L N G K G A P R R G Q K T R R K N T  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|  
CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++| 525  
GACGAGTGAAAGAAGTTACCACCATGTGAGTATC  
S A H F L P M V V H S  
|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|

FIG.24B





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ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAAACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

MTQCALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVWRKLFSTKYFLKIE  
KNGKVSGETTKENCYPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL  
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVS.

## FIG.25

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTGTTGGCGT  
AACTGTTCTCTTTCACCAAATACTTCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATA  
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA  
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAACGAAGG  
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRIHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSGETTKENCYPYSILEITSVEIGV  
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVVS.

## FIG.26



... ..

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ATGGTTCGTTGGCGTAAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAA  
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATA  
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTA  
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAATGACTGTAAG  
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG  
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA  
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA  
TAG

MVRWRKLFSTKYFLKIEKNGKVSgtKKENCpYSILEITSVEIGVVAVKAINSnyyLAM  
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR  
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCAT  
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA  
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAAC  
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC  
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG  
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA  
ATGGTGGTACACTCATAG

MEKNGKVSgtKKENCpYSILEITSVEIGVVAVKAINSnyyLAMNKKGKLYGSKEFNND  
CKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH  
S.

FIG.28



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ATGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT  
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC  
TCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA  
AATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCCAAATGTA  
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA  
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGY  
NTYASFNWOHNGROMYVALNGKGAPRRGOKTRRKNTSAHFLPMVVS.

## FIG. 29

ATGGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT  
CTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA  
ATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCCAAATGTAT  
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAA  
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY  
VALNGKGAPRRGOKTRRKNTSAHFLPMVVHS.

## FIG. 30

ATGGGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG  
GATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA  
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA  
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT  
RRKNTSAHFLPMVVHS.

## FIG. 31



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ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTACGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE  
KNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSNNYLLAMNKKGKLYGSKEFNNDCKL  
K

FIG.32

ATGGCTGGTCGTACGTTGTTCTTACAACCACCTGCAGGGTGACGTTGTTGGCGT  
AACTGTTCTCTTTCACCAAATACTTCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGV  
VAVKAINSNNYLLAMNKKGKLYGSKEFNNDCKLK

FIG.33



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C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCAC  
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCAC  
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAAGAATTTAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.35



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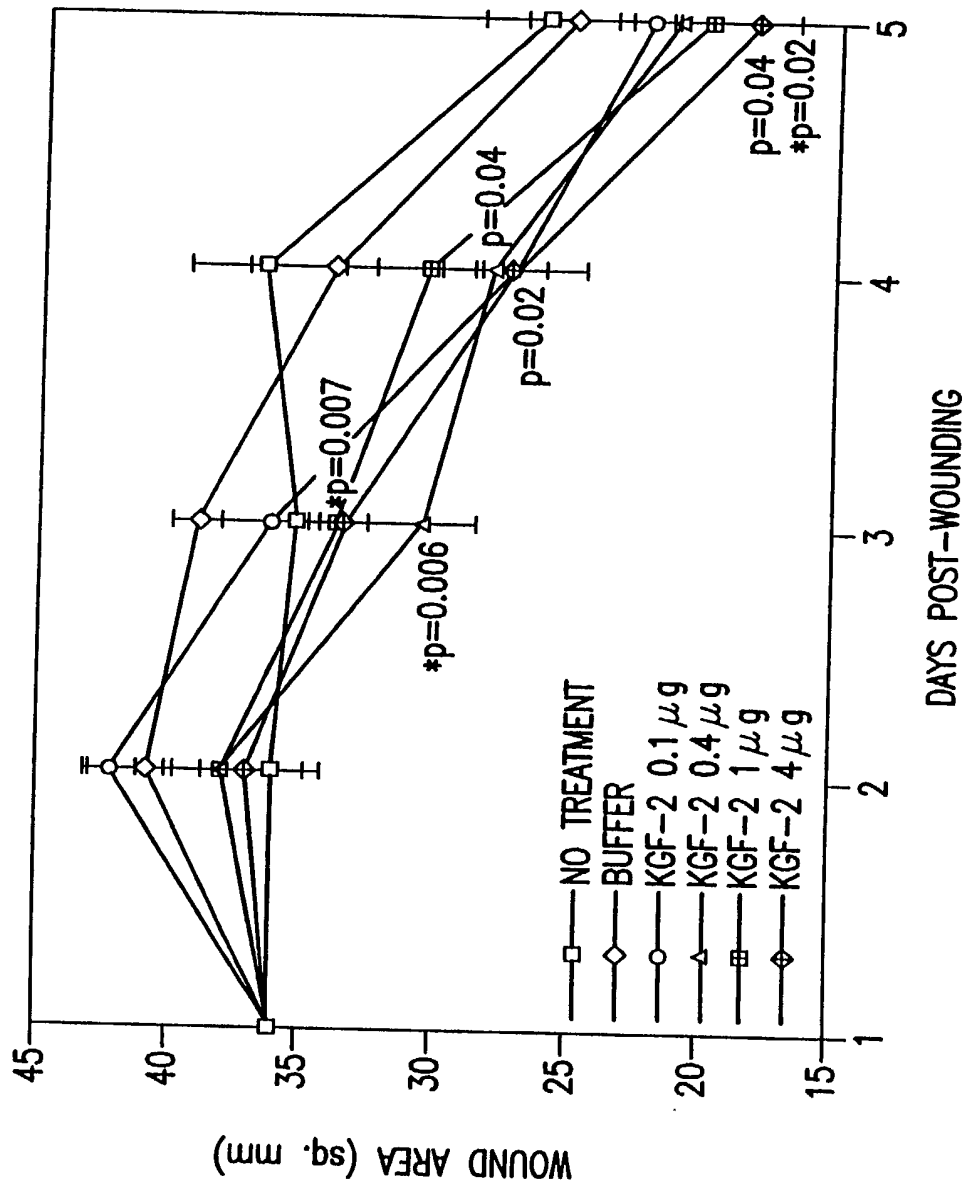


FIG.36



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# EFFECT OF KGF-2 Δ33 ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9±2.5	58.8±3.7	6.8±0.2	1142±141	3.8±0.4
BUFFER	25.1±1.7	60.2±2.6	6.4±0.2	923±61	5.0±0.4
KGF-2/Δ33 (0.1μg)	22.0±0.9	65±1.4	6.8±0.2	1275±148	4.6±0.7
KGF-2/Δ33 (0.4 μg)	21.1±1.4	68.4±2.4	8.0±0.5 p=0.0445*	1310±182	4.2±0.7
KGF-2/Δ33 (1.0 μg)	19.9±1.5	66.2±2.1	8.4±0.4 p=0.0159* p=0.0053†	1389±115 p=0.0074†	3.3±0.25 p=0.0217†
KGF-2/Δ33 (4.0μg)	18.1±1.6 p=0.0398* p=0.0200†	71.2±2.6 p=0.0367* p=0.0217†	8.5±0.3 p=0.0047* p=0.0445†	1220±89 p=0.0254†	5.3±0.9

FIG.37



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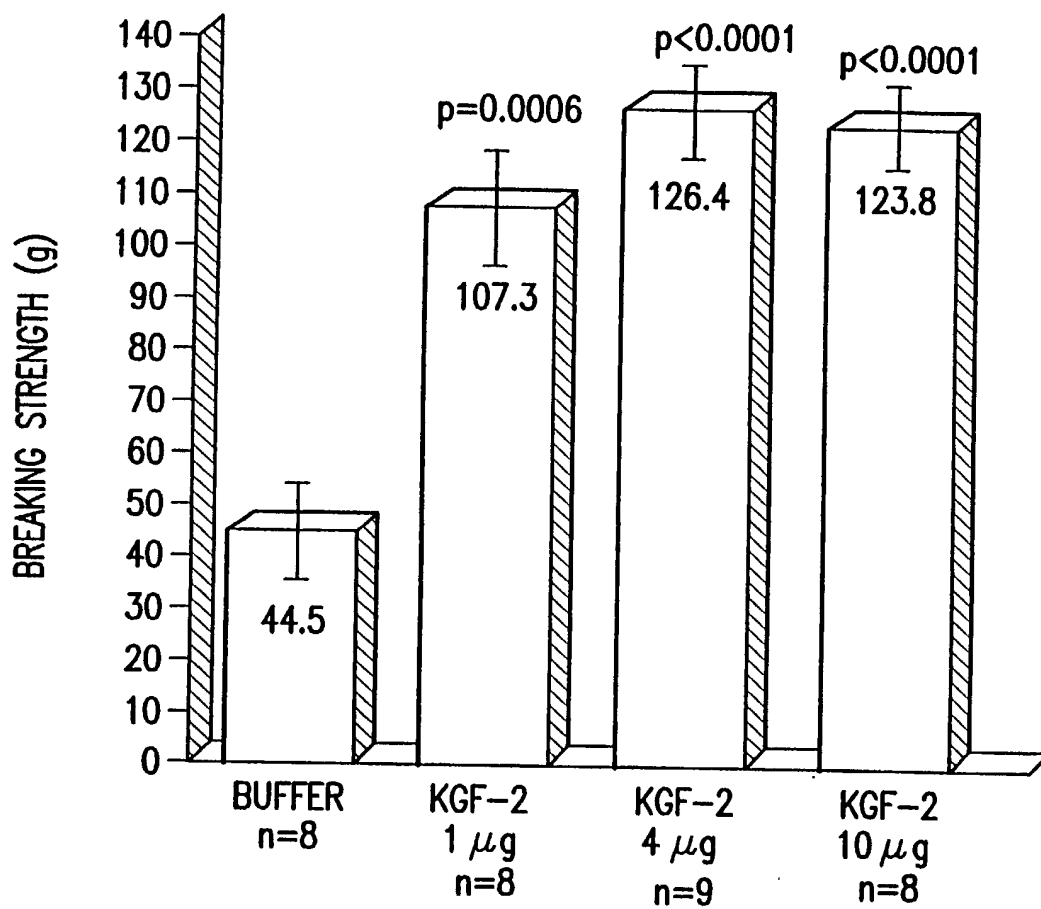


FIG.38





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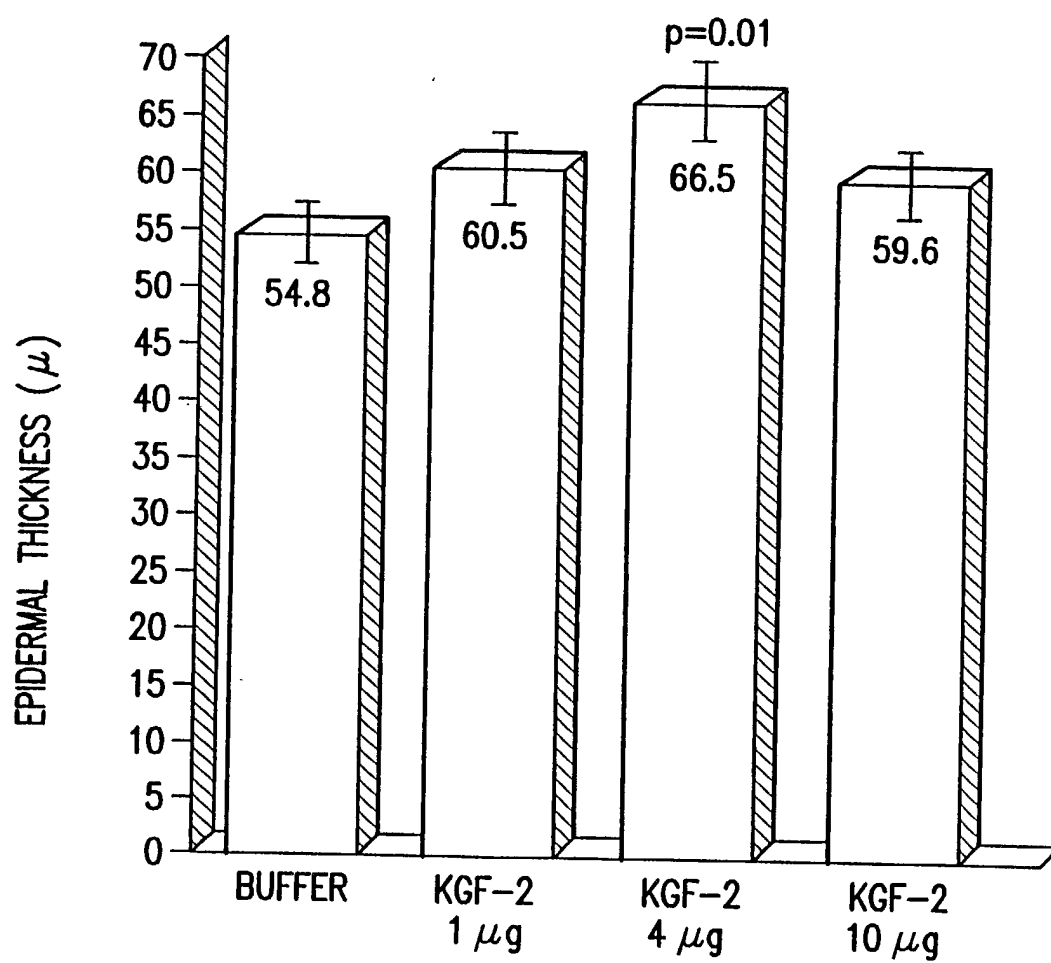


FIG.39



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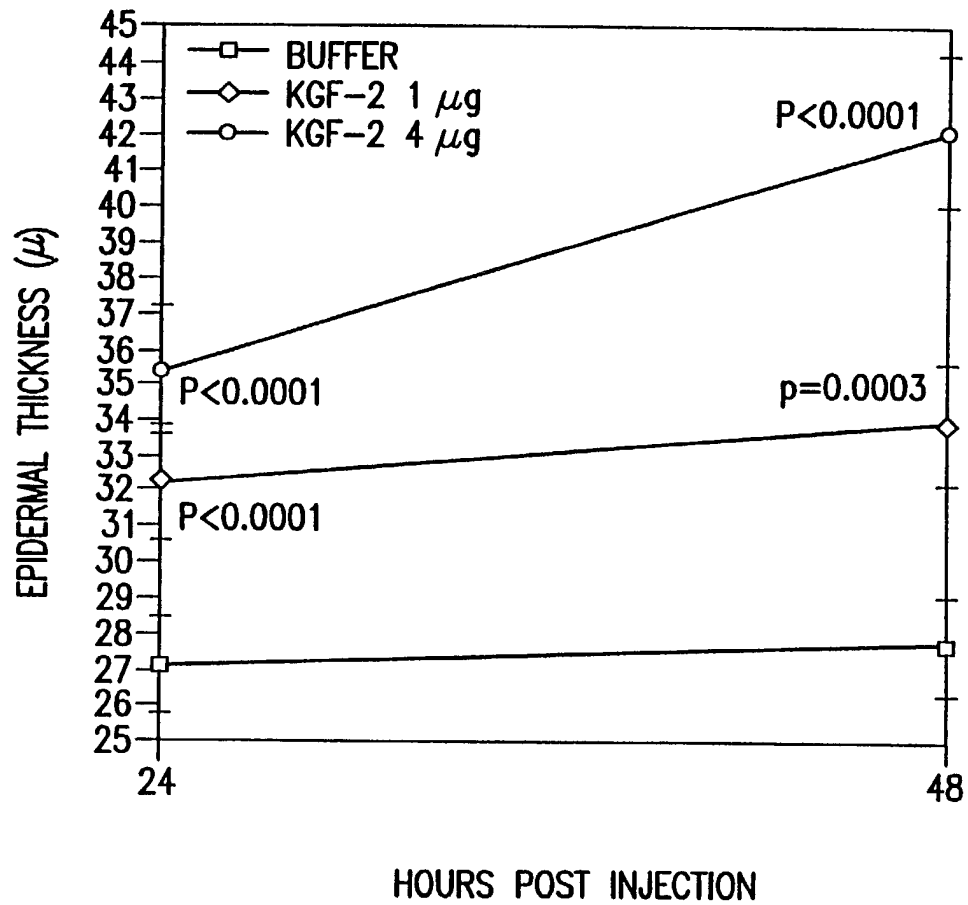


FIG.40



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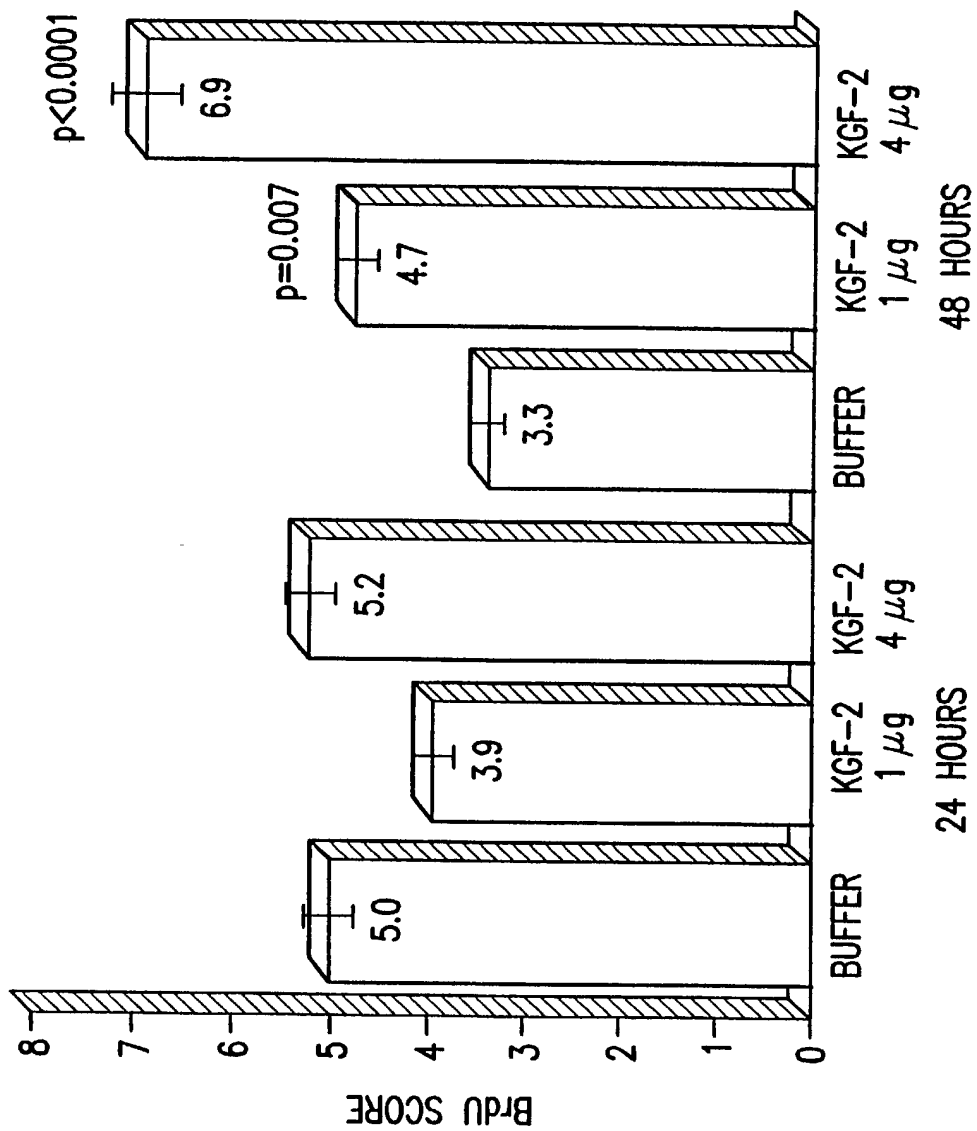


FIG.41

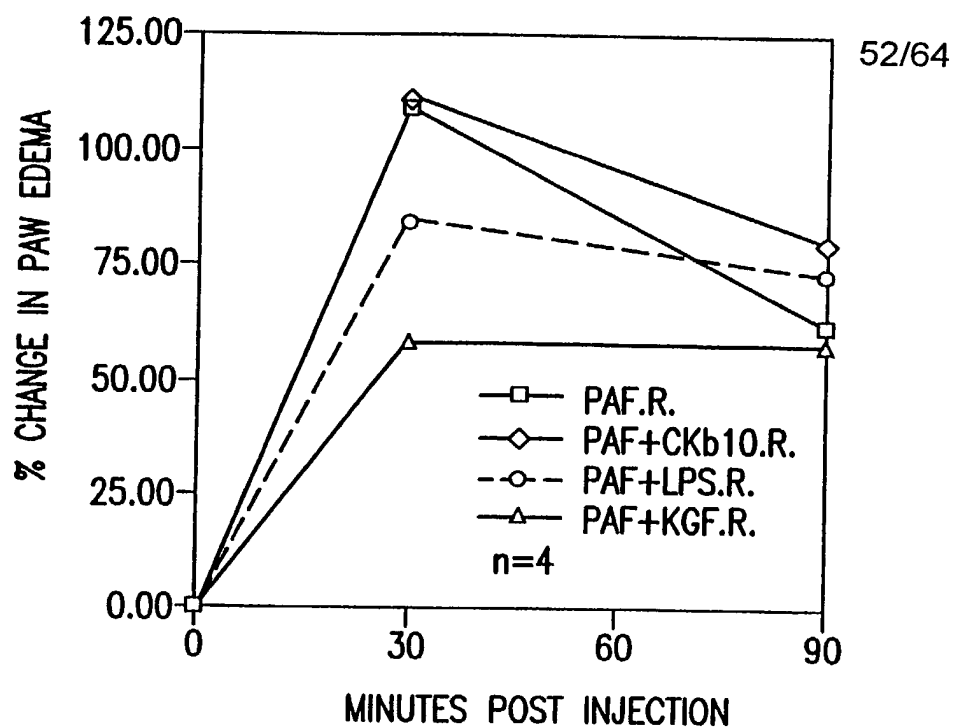


FIG.42A

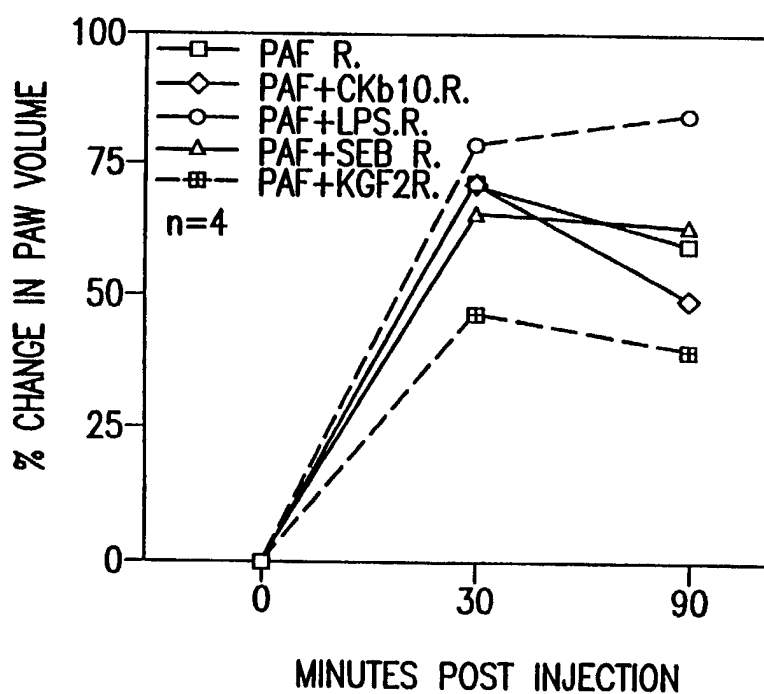


FIG.42B



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EFFECT OF KGF-2  $\Delta 33$  ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

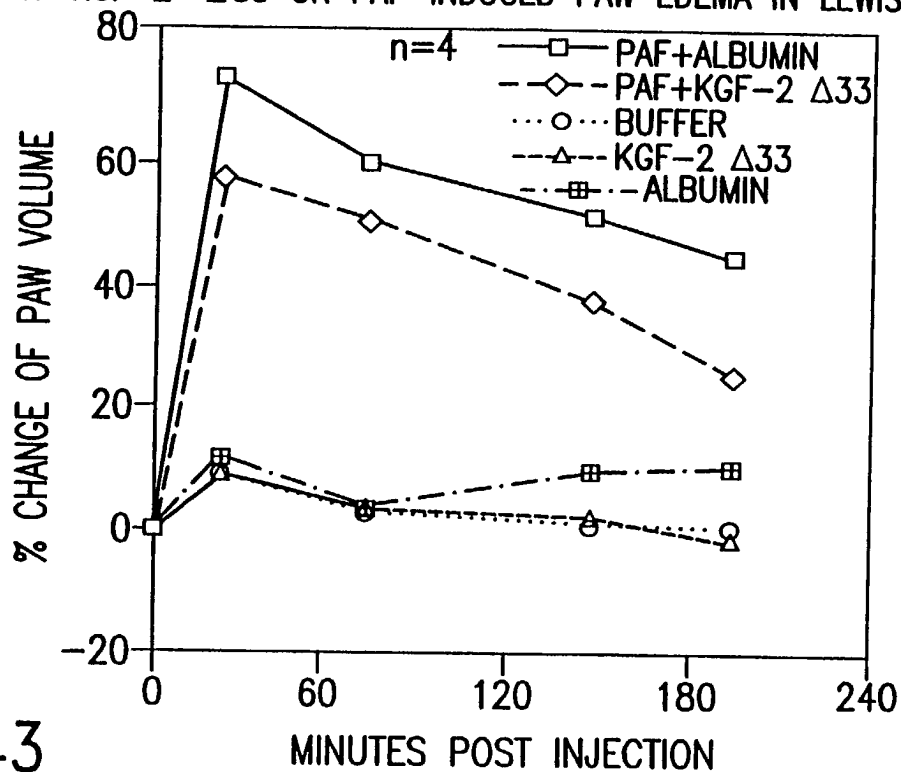


FIG.43

EFFECT OF KGF-2  $\Delta 33$  ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

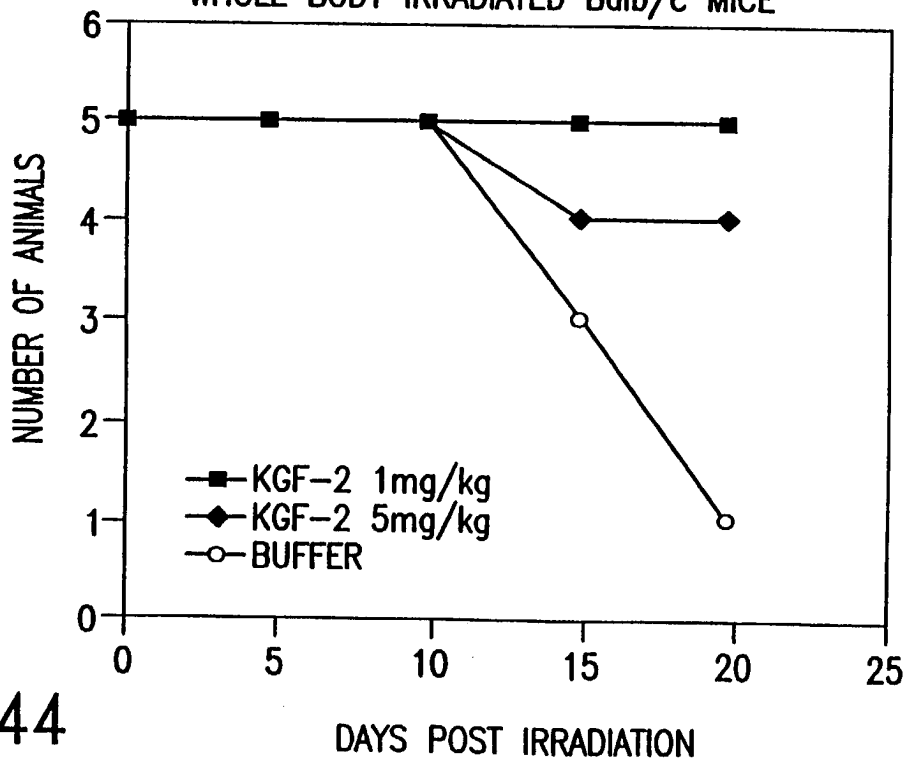
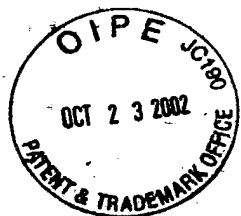


FIG.44



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# EFFECT OF KGF-2 $\Delta$ 33 ON BODY WEIGHT OF IRRADIATED MICE

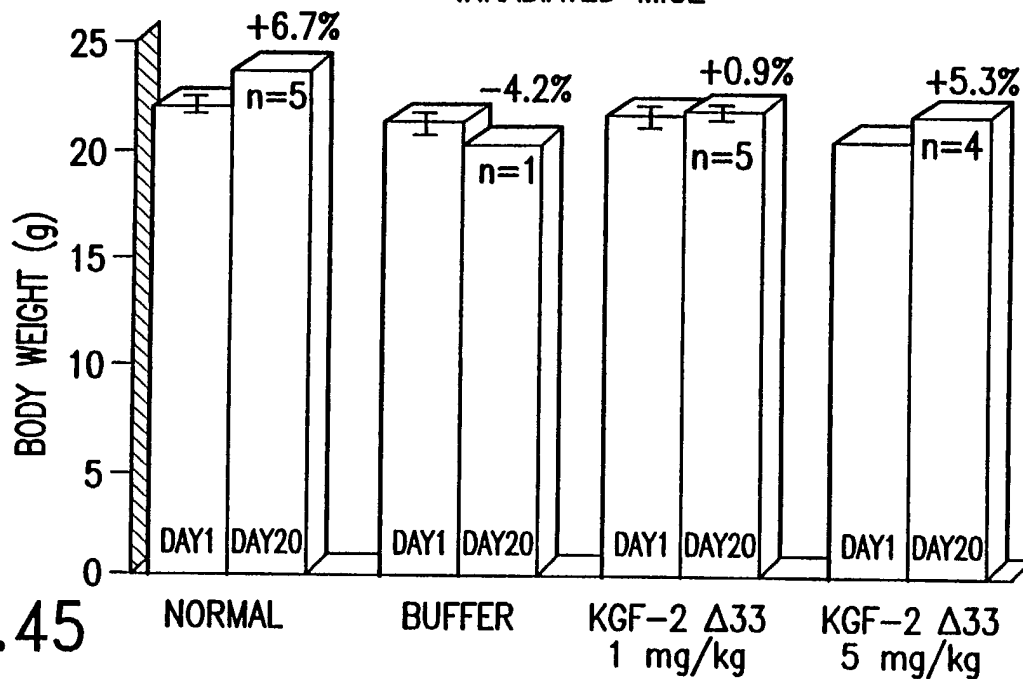


FIG.45

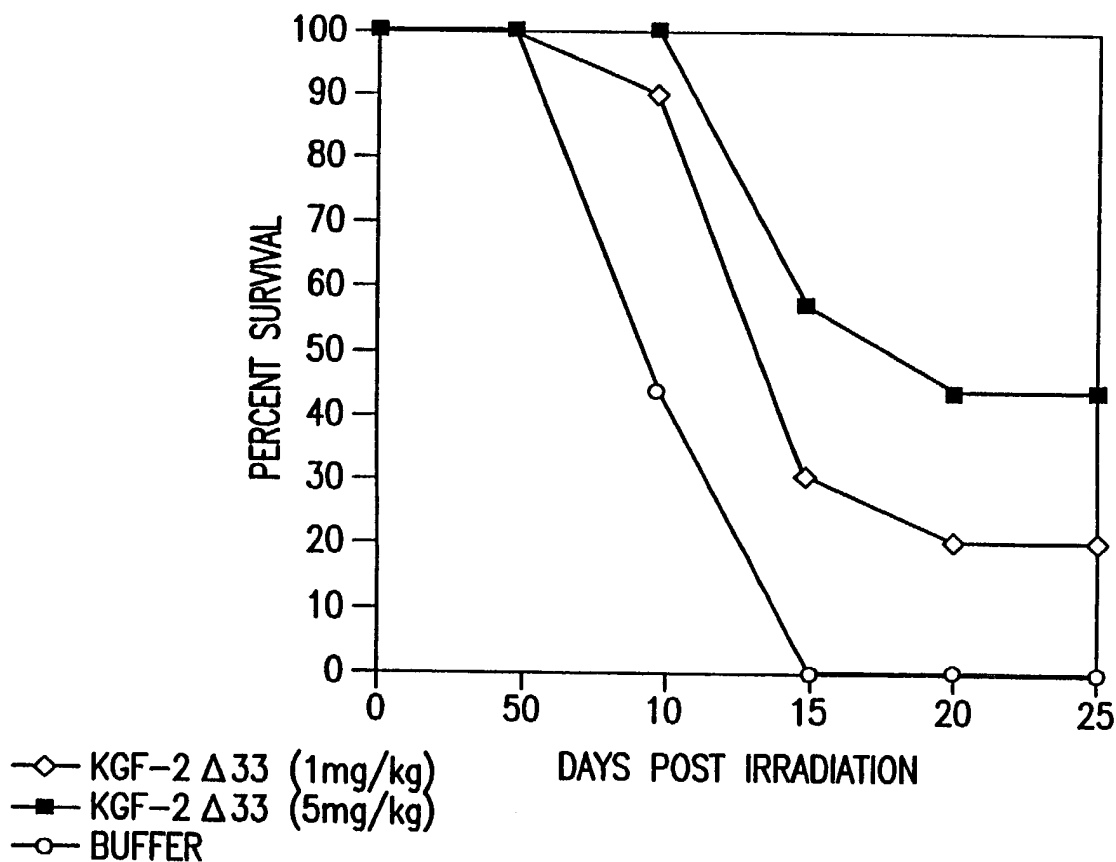


FIG.46



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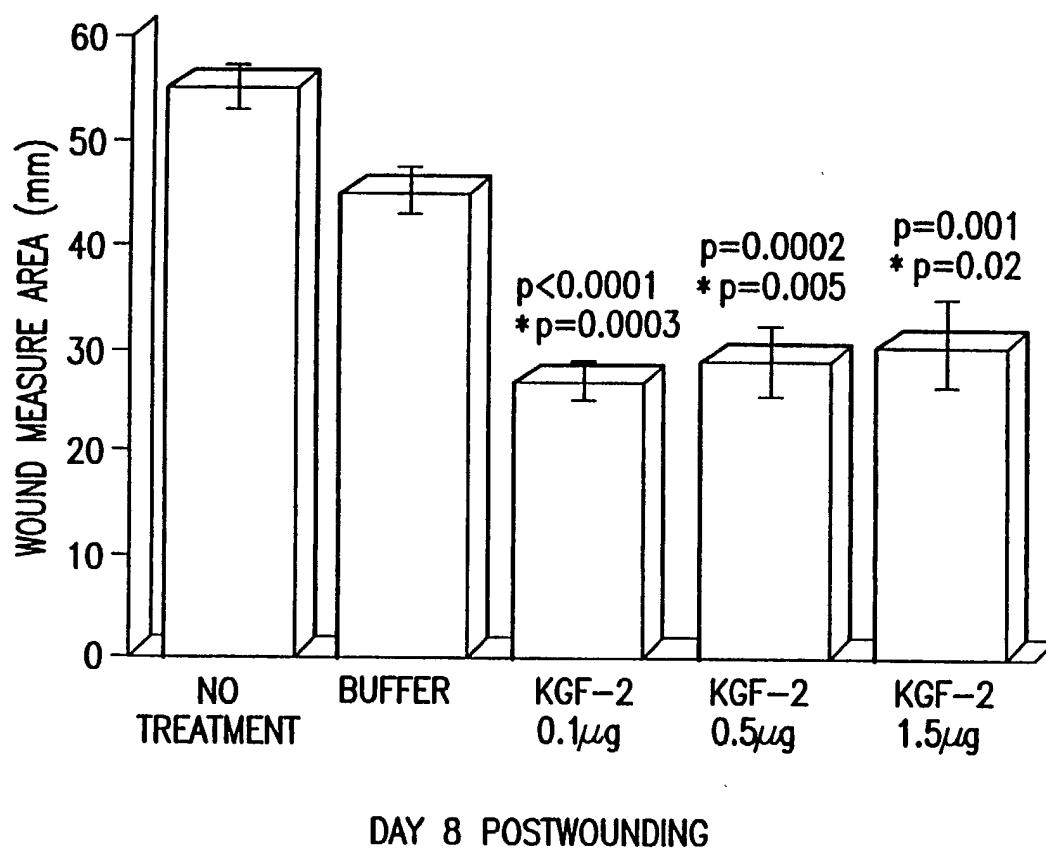


FIG.47



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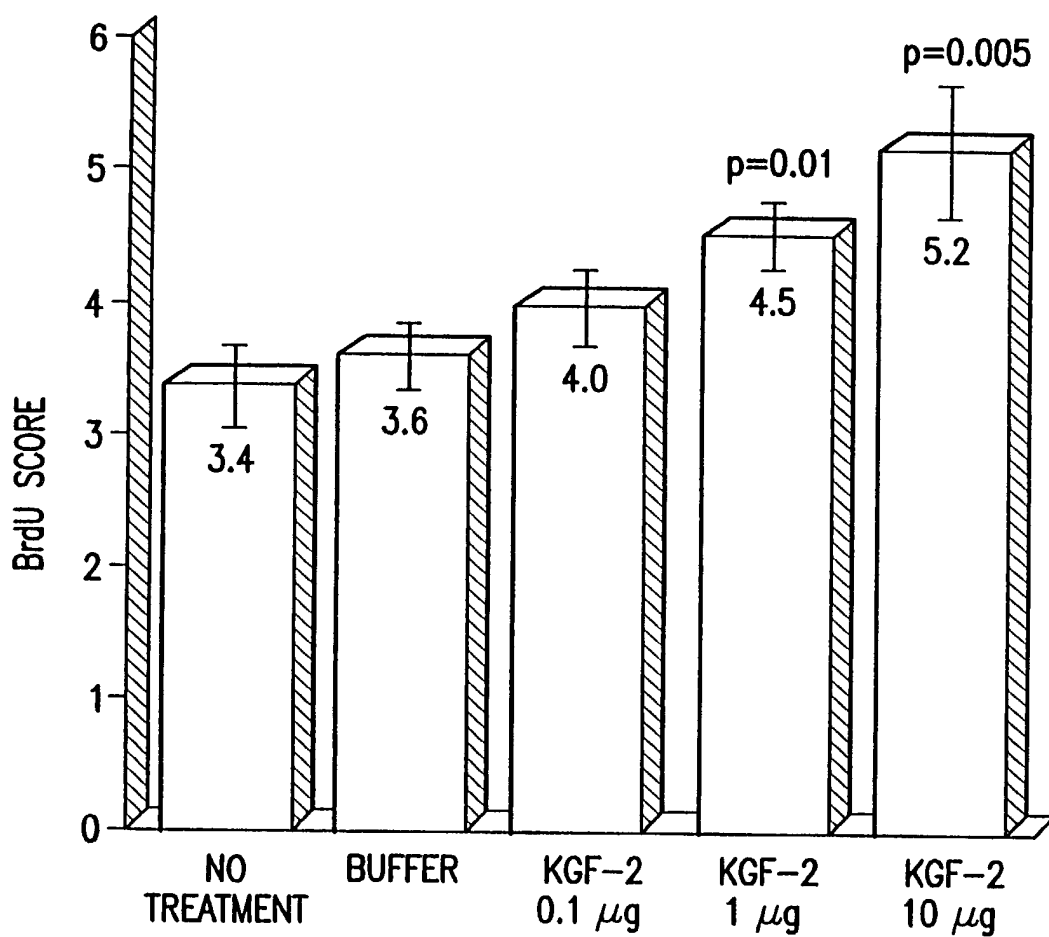


FIG.48





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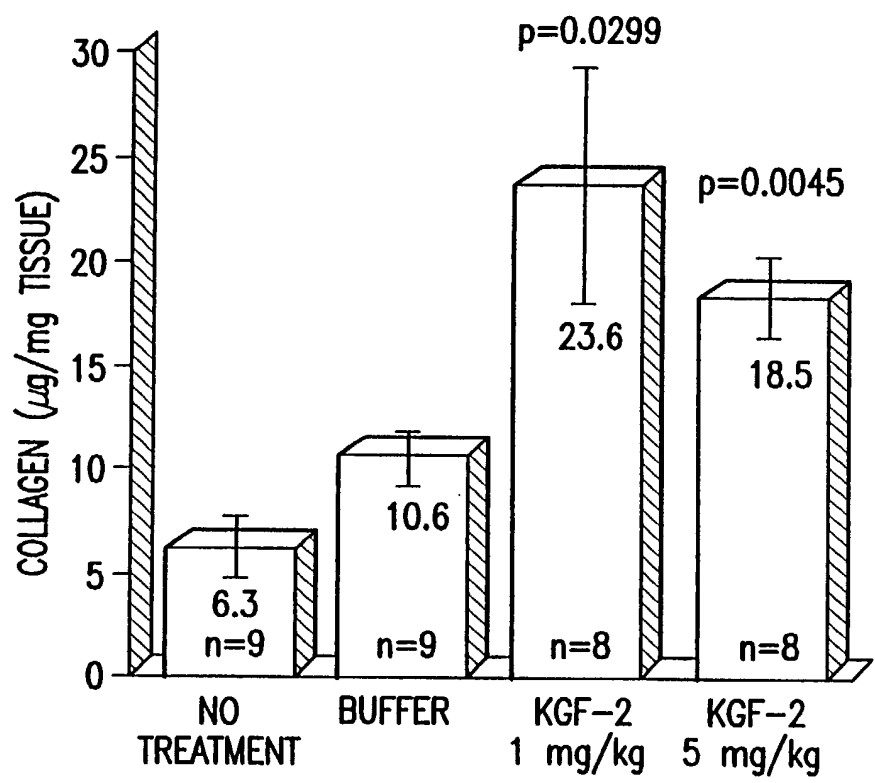


FIG.49



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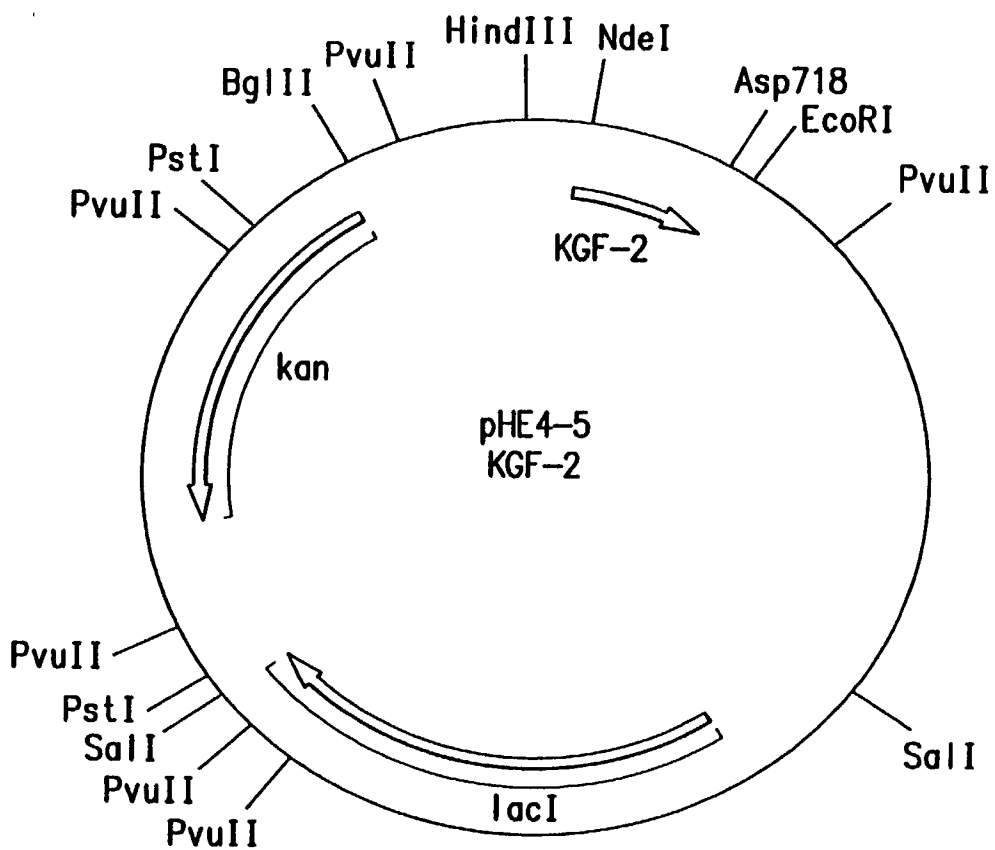


FIG. 50

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1      AAGCTTAAAAAACTGCAAAAAATAGT <sup>-35</sup> TTGACT(TGTGAGCGGATAACAAT)      Operator 1

50      <sup>-10</sup> TAAGATGTACCCA ATTGTGAGCGGATAACAATTCACACATTAA      Operator 2

94      <sup>S/D</sup> AGAGGAGAAATTA CATATG

FIG. 51



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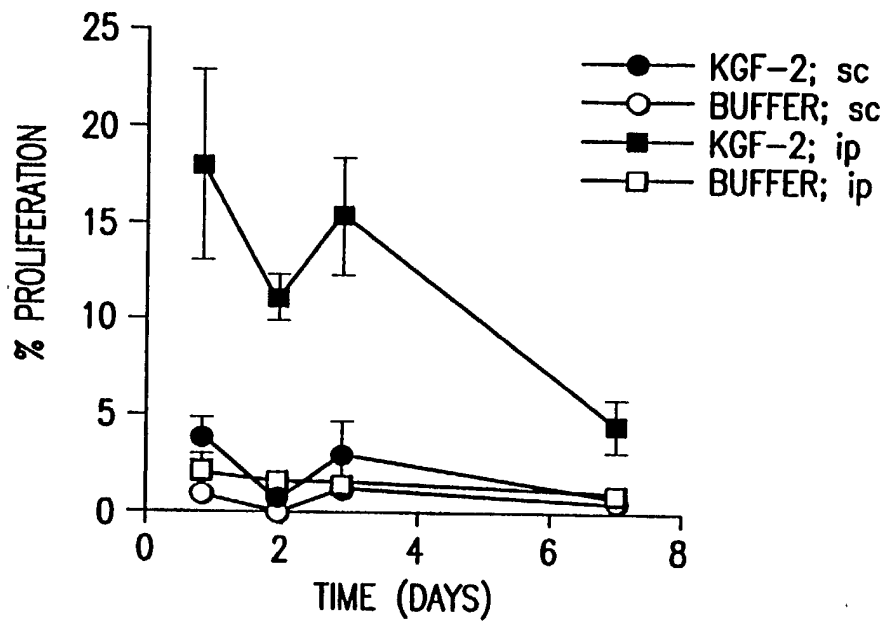


FIG. 52

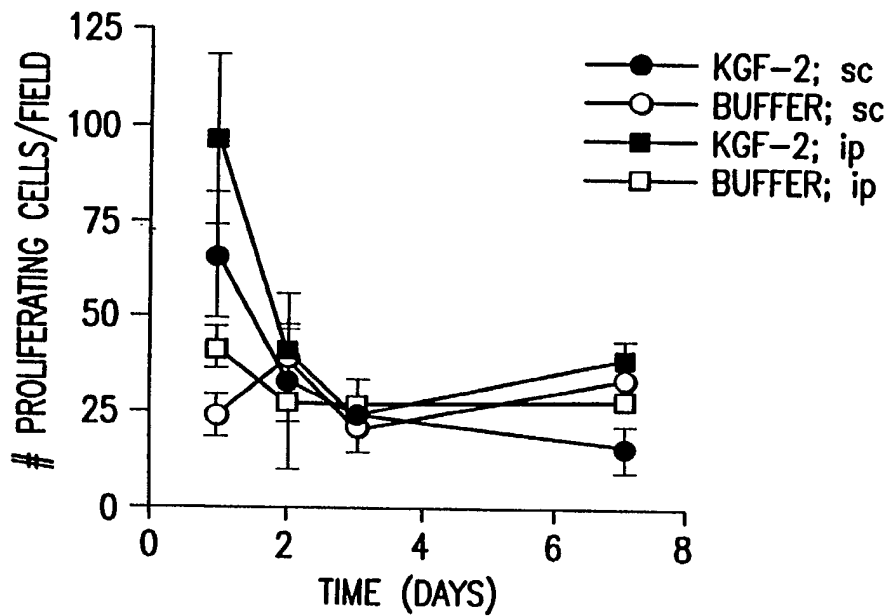
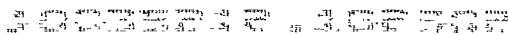


FIG. 53



Group	Percent Ulceration (approx.)	p-value (vs BUFFER)
SALINE CONTROL	1	
BUFFER	37	
KGF-2 1 mg/kg	1	0.0128
KGF-2 5 mg/kg	4.5	0.0338

Group	Bladder Wall Thickness (approx.)	Significance (vs. Buffer)
SALINE CONTROL	40	
BUFFER	210	
KGF-2 1 mg/kg	100	$p = 0.0077$
KGF-2 5 mg/kg	50	$p < 0.0001$

FIG. 55



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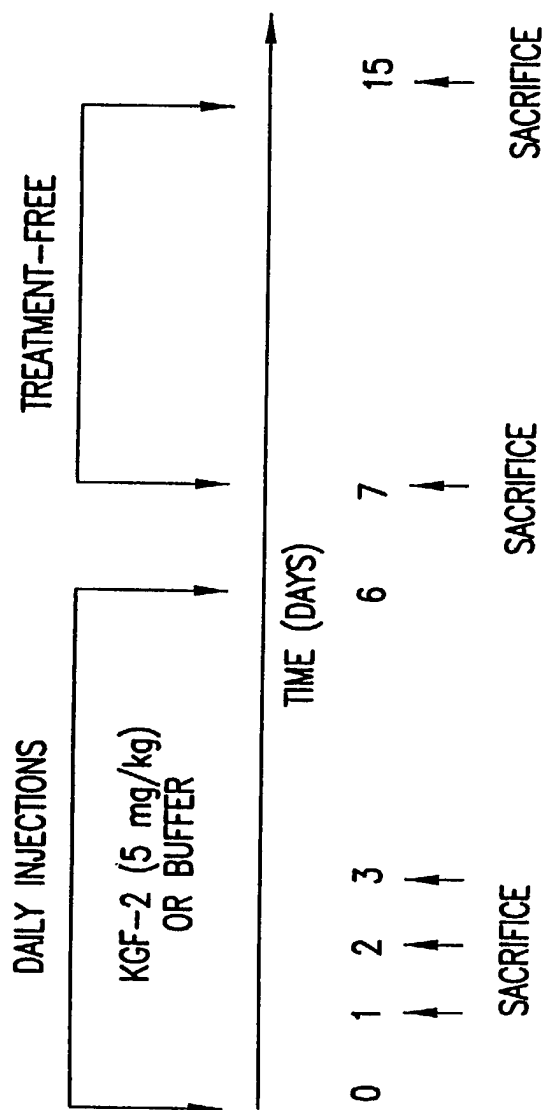


FIG. 56



U.S. PATENT & TRADEMARK OFFICE

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2 63/64

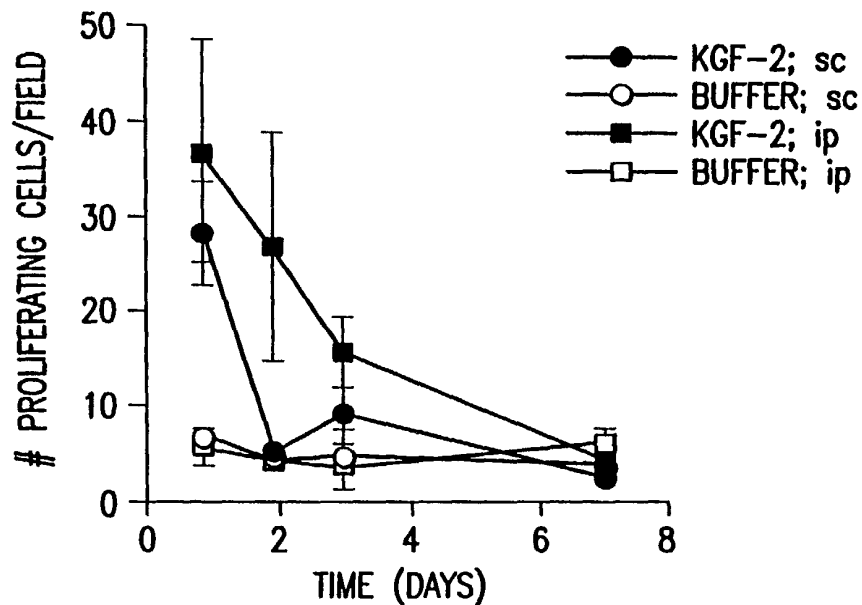


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

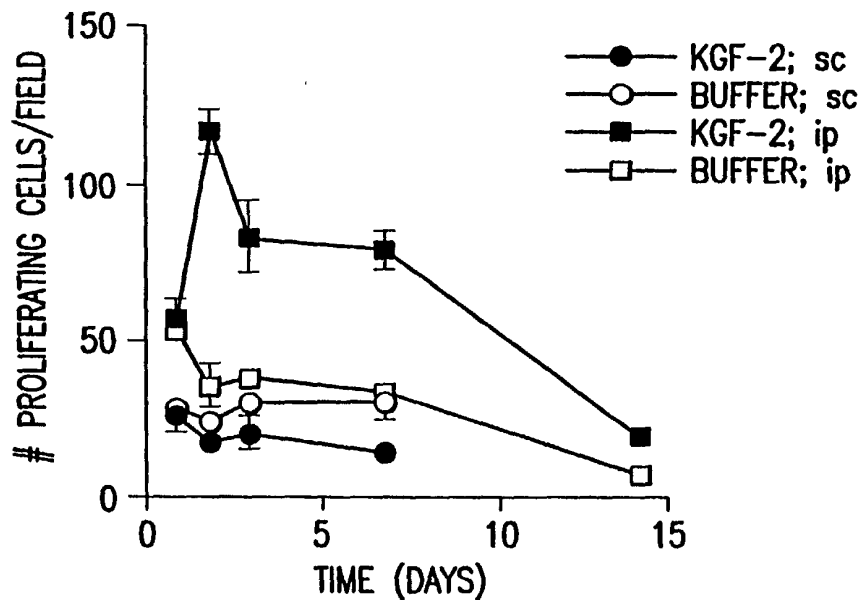


FIG. 58



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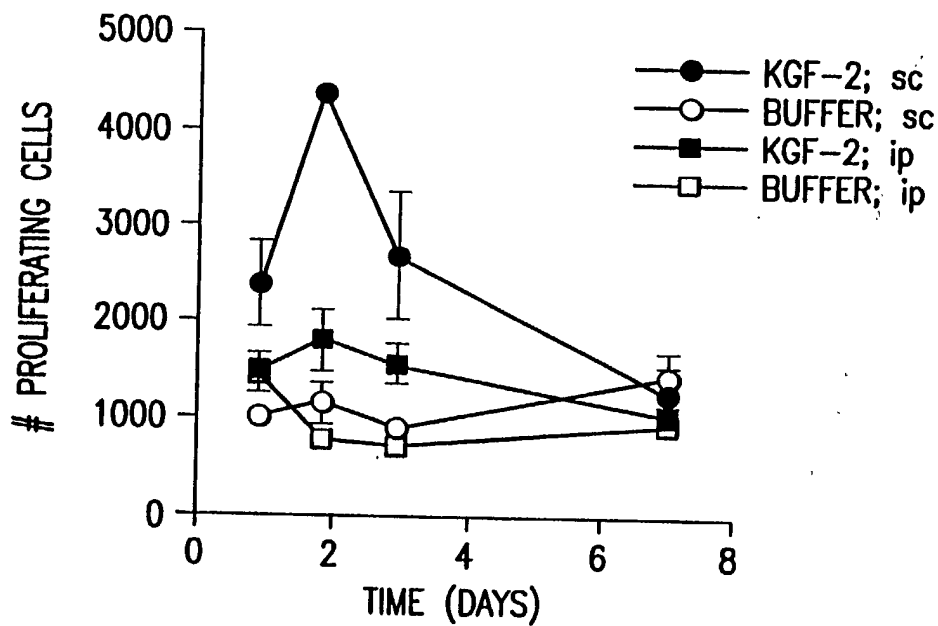


FIG. 59

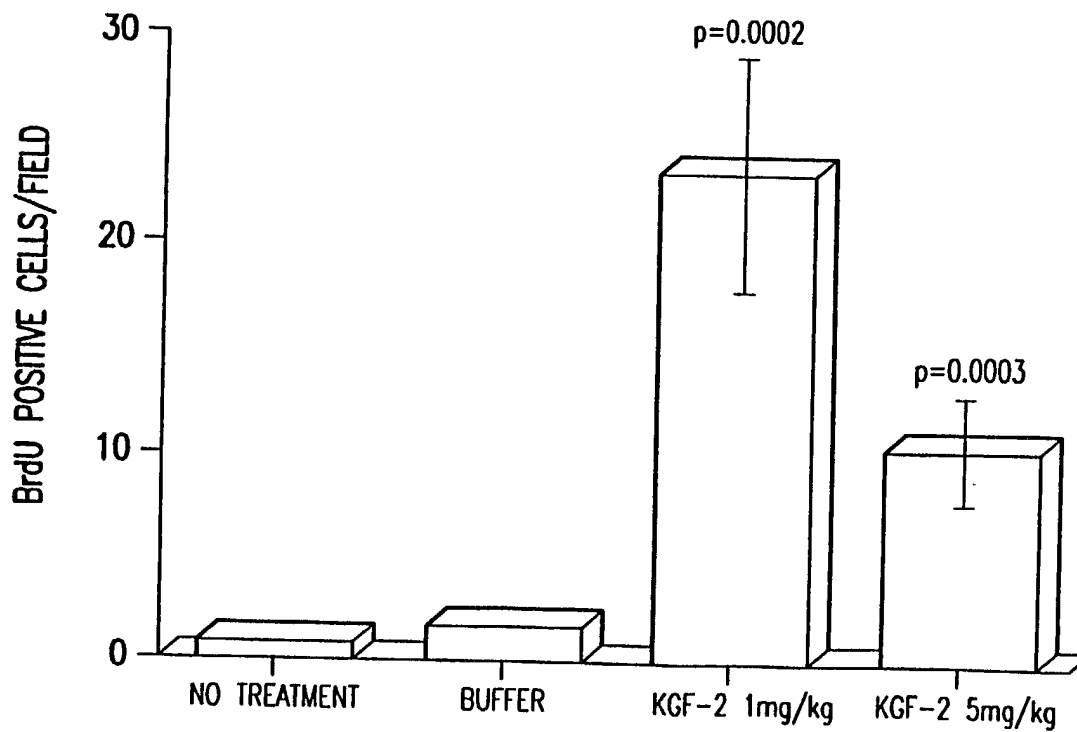


FIG. 60